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OM protein - protein search, using sw model.

Run on: July 28, 2003, 17:04:20 ; Search time 13 Seconds
(without alignments)
3.159 Million cell updates/sec

Title: US-09-930-125-3
Perfect score: 54
Sequence: 1 EEVLVPOQGF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 41799 seqs, 4106219 residues

Total number of hits satisfying chosen parameters: 41799

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New.*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	1255	1 PCT-US03-20322-213	Sequence 213, App
2	35	64.8	453	6 US-10-273-573-7709	Sequence 7709, App
3	35	64.8	474	6 US-10-273-573-9017	Sequence 9017, App
4	33	61.1	1224	1 PCT-US02-41730-2	Sequence 2, Appli
5	32	59.3	180	6 US-10-294-433-421	Sequence 421, App
6	31	57.4	245	6 US-10-273-573-6289	Sequence 6289, App
7	31	57.4	532	6 US-10-294-433-388	Sequence 388, App
8	31	57.4	1261	6 US-10-273-573-7512	Sequence 7512, App
9	31	57.4	2662	6 US-10-273-573-8548	Sequence 8548, App
10	31	57.4	2703	6 US-10-273-573-8538	Sequence 8538, App
11	31	57.4	2719	6 US-10-273-573-8996	Sequence 8996, App
12	31	57.4	2986	6 US-10-273-573-8550	Sequence 8550, App
13	31	57.4	3114	6 US-10-273-573-8546	Sequence 8546, App
14	31	57.4	3509	6 US-10-273-573-8544	Sequence 8544, App
15	31	57.4	4766	6 US-10-273-573-8539	Sequence 8539, App
16	31	57.4	4367	6 US-10-273-573-8549	Sequence 8549, App
17	31	57.4	5367	6 US-10-273-573-8547	Sequence 8547, App
18	30	55.6	221	6 US-10-273-573-6685	Sequence 6685, App
19	30	55.6	547	7 US-60-478-196-3018	Sequence 3018, App
20	30	55.6	670	7 US-60-478-196-3311	Sequence 3311, App
21	29	53.7	207	1 PCT-US03-20041-105	Sequence 105, App
22	29	53.7	257	6 US-10-273-573-5844	Sequence 5844, App
23	29	53.7	303	6 US-10-273-573-5845	Sequence 5845, App
24	29	53.7	349	1 PCT-US03-20041-80	Sequence 80, Appl
25	29	53.7	351	1 PCT-US03-20041-82	Sequence 82, Appl
26	29	53.7	351	1 PCT-US03-20041-91	Sequence 91, Appl

ALIGNMENTS

RESULT 1
PCT-US03-20322-213
; Sequence 213, Application PC/YUS0320322
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; FILE REFERENCE: DPN-043PC
; CURRENT APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR FILING DATE: 2003-06-27
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 213
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-20322-213

Query Match 100.0%; Score 54; DB 1; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	EEVLVPOQGF	10
DB	1021	EEVLVPOQGF	1030

RESULT 2
US-10-273-573-7709
; Sequence 7709, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066 US/10/273,573
; CURRENT APPLICATION NUMBER: US/10/273,573
; PRIOR FILING DATE: 2002-10-18
; PRIOR FILING DATE: 2002-10-18
; PRIOR FILING DATE: 2000-04-18
; PRIOR FILING DATE: 2000-04-18
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 7709
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

Sequence 110, App
Sequence 99, Appl
Sequence 6, Appli
Sequence 5843, Ap
Sequence 7295, Ap
Sequence 11, Appl
Sequence 13, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 10219, A
Sequence 4, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 5, Appli
Sequence 18, Appl
Sequence 36, Appl
Sequence 45, Appl
Sequence 9500, Ap
Sequence 8835, Ap

NAME/KEY: DOMAIN
LOCATION: (168)...(183)
OTHER INFORMATION: G-PROTEIN BETA WD-40 REPEAT SIGNATURE domain identified by
OTHER INFORMATION: eMATRIX, accession number PR00320A, p-value=1.000e-10, raw score
OTHER INFORMATION: 16.74
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (96)...(181)
OTHER INFORMATION: WD domain, G-beta repeat domain identified by Pfam, accession
OTHER INFORMATION: name WD40, E-value=1.1e-05, Pfam score of 32.3
US-10-273-573-7709

Query Match 64.8%; Score 35; DB 6; Length 453;
Best Local Similarity 50.0%; Pred. No. 9.1;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEYLVPOQGF 10
:|:|:|:|:
DB 300 DEHLIPOLGY 309

RESULT 3

US-10-273-573-9017
Sequence 9017, Application US/10273573
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
CURRENT APPLICATION NUMBER: US/10/273,573
PRIOR FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 10994
SOFTWARE: Custom
SEQ ID NO 9017
LENGTH: 474
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (189)...(204)
OTHER INFORMATION: G-PROTEIN BETA WD-40 REPEAT SIGNATURE domain identified by
OTHER INFORMATION: eMATRIX, accession number PR00320A, p-value=1.000e-10, raw score
OTHER INFORMATION: 16.74
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (117)...(202)
OTHER INFORMATION: WD domain, G-beta repeat domain identified by Pfam, accession
OTHER INFORMATION: name WD40, E-value=1.1e-05, Pfam score of 32.3
US-10-273-573-9017

Query Match 64.8%; Score 35; DB 6; Length 474;
Best Local Similarity 50.0%; Pred. No. 9.5;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEYLVPOQGF 10
:|:|:|:|:
DB 321 DEHLIPOLGY 330

RESULT 4

PCT-US02-41730-2
Sequence 2, Application PC/TUS0241730
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: AGGREGANASE MOLECULES
FILE REFERENCE: AM100884 PCT
CURRENT APPLICATION NUMBER: PCT/US02/41730
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: 60/344,895
PRIOR FILING DATE: 2001-12-31

NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 1224
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-41730-2

Query Match 61.1%; Score 33; DB 1; Length 1224;
Best Local Similarity 85.7%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YLVPQOG 9
|:|:|:|:
DB 1198 YLVPQHG 1204

RESULT 5

US-10-294-433-421
Sequence 421, Application US/10294433
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 792CIP4
CURRENT APPLICATION NUMBER: US/10/294,433
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: PCT/US01/14826
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/989,600
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 09/577,408
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: 10/115,831
PRIOR FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: 09/677,298
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/695,781
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 10/150,802
PRIOR FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: 09/715,869
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 10/167,379
PRIOR FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 09/775,330
PRIOR FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 864
SOFTWARE: Custom
SEQ ID NO 421
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
US-10-294-433-421

Query Match 59.3%; Score 32; DB 6; Length 180;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEYLVPOQG 9
|:|:|:|:
DB 60 EEWLAPVQG 68

RESULT 6

US-10-273-573-6289
Sequence 6289, Application US/10273573
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522,929

; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 6289
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(245)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-273-573-6289

Query Match 57.4%; Score 31; DB 6; Length 245;
Best Local Similarity 55.6%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EYLVPOQG 9
| | | : | : |
Db 196 EYQIPEVG 204

RESULT 7

US-10-294-433-388
; Sequence 388, Application US/10294433
; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 792CIP4
; CURRENT APPLICATION NUMBER: US/10/294,433
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/US01/14826
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/989,600
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/577,408
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 10/115,831
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/677,298
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/695,781
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 10/150,802
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 09/715,869
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 10/167,379
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/775,330
; PRIOR FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 864
; SOFTWARE: Custom
; SEQ ID NO 388
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-294-433-388

Query Match 57.4%; Score 31; DB 6; Length 532;
Best Local Similarity 55.6%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EYLVPOQG 9
| | | : | : |
Db 505 EYLIPIVAG 513

RESULT 8

US-10-273-573-7512
; Sequence 7512, Application US/10273573

; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 7512
; LENGTH: 1261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-273-573-7512

Query Match 57.4%; Score 31; DB 6; Length 1261;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LVPOQGF 10
| | | : | : |
Db 435 LLPEQGF 441

RESULT 9

US-10-273-573-8548
; Sequence 8548, Application US/10273573
; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 8548
; LENGTH: 2662
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: DOMAIN
; LOCATION: (1002)...(2138)
; OTHER INFORMATION: BRCA2 repeat domain identified by Pfam, accession name
; OTHER INFORMATION: BRCA2_repeat, E-value=2e-111, Pfam score of 383.6
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2662)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-273-573-8548

Query Match 57.4%; Score 31; DB 6; Length 2662;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 EYLVPOQGF 10
| | | : | : |
Db 2089 EHLISQKGF 2097

RESULT 10

US-10-273-573-8538
; Sequence 8538, Application US/10273573
; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066

; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 8538
; LENGTH: 2703
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1026)..(1064)
; OTHER INFORMATION: S-adenosyl-L-homocysteine hydrolase proteins domain
; OTHER INFORMATION: identified by eMATRIX, accession number BL00738C, p-value=9.357e-
; OTHER INFORMATION: 09, raw score of 16.53
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (3)..(2576)
; OTHER INFORMATION: BRCA2 repeat domain identified by Pfam, accession name
; OTHER INFORMATION: BRCA2_repeat, E-value=3.2e-106, Pfam score of 366.3

US-10-273-573-8538

Query Match 57.4%; Score 31; DB 6; Length 2703;

Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EYLVPQOGF 10

Db 365 EHLISQKGF 373

RESULT 11

US-10-273-573-8996
; Sequence 8996, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 8996
; LENGTH: 2719
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (2481)..(2526)
; OTHER INFORMATION: Amino acid permeases proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL002118D, p-value=8.043e-37, raw score of 21.49
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1215)..(1561)
; OTHER INFORMATION: Cell cycle protein domain identified by Pfam, accession name
; OTHER INFORMATION: FTSW_RODA_SPOVE, E-value=1e-80, Pfam score of 281.6

US-10-273-573-8996

Query Match 57.4%; Score 31; DB 6; Length 2719;

Best Local Similarity 62.5%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YLVPQOGF 10

Db 2621 YLLPQKAF 2628

RESULT 12

US-10-273-573-8550
; Sequence 8550, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 8550
; LENGTH: 2986
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (2946)..(2984)
; OTHER INFORMATION: S-adenosyl-L-homocysteine hydrolase proteins domain
; OTHER INFORMATION: identified by eMATRIX, accession number BL00738C, p-value=9.
; OTHER INFORMATION: 09, raw score of 16.53
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (92)..(2335)
; OTHER INFORMATION: BRCA2 repeat domain identified by Pfam, accession name
; OTHER INFORMATION: BRCA2_repeat, E-value=6.2e-162, Pfam score of 551.4
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2986)
; OTHER INFORMATION: xaa = x or * as defined in Table 2

US-10-273-573-8550

Query Match 57.4%; Score 31; DB 6; Length 2986;

Best Local Similarity 55.6%; Pred. No. 3.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EYLVPQOGF 10

Db 2286 EHLISQKGF 2294

RESULT 13

US-10-273-573-8546
; Sequence 8546, Application US/10273573
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 8546
; LENGTH: 3114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (2551)..(2589)
; OTHER INFORMATION: S-adenosyl-L-homocysteine hydrolase proteins domain
; OTHER INFORMATION: identified by eMATRIX, accession number BL00738C, p-value=9.
; OTHER INFORMATION: 09, raw score of 16.53
; FEATURE:
; NAME/KEY: DOMAIN

; LOCATION: (1002)..(1938)
; OTHER INFORMATION: BRCA2 repeat domain identified by Pfam, accession name
; OTHER INFORMATION: BRCA2_repeat, E-value=9.6e-108, Pfam score of 371.4
US-10-273-573-8546

Query Match 57.4%; Score 31; DB 6; Length 3114;
Best Local Similarity 55.6%; Pred. No. 4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EYLVPQOGF 10
|:|: |:|
Db 1890 EHLISQKGF 1898

RESULT 14

US-10-273-573-8544
; Sequence 8544, Application US/10273573
; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 8544
; LENGTH: 3509
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: DOMAIN
; LOCATION: (716)..(3025)
; OTHER INFORMATION: BRCA2 repeat domain identified by Pfam, accession name
; OTHER INFORMATION: BRCA2_repeat, E-value=1.8e-192, Pfam score of 652.8
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(3509)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-273-573-8544

Query Match 57.4%; Score 31; DB 6; Length 3509;
Best Local Similarity 55.6%; Pred. No. 4.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EYLVPQOGF 10
|:|: |:|
Db 2977 EHLISQKGF 2985

RESULT 15

US-10-273-573-8539
; Sequence 8539, Application US/10273573
; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: US/10/273,573
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom
; SEQ ID NO 8539
; LENGTH: 4766
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: DOMAIN
; LOCATION: (1732)..(1770)
; OTHER INFORMATION: S-adenosyl-L-homocysteine hydrolase proteins domain
; OTHER INFORMATION: identified by eMATRIX, accession number BL00738C, p-value=9.35
; OTHER INFORMATION: 09, raw score of 16.53
; FEATURE:

; NAME/KEY: DOMAIN
; LOCATION: (694)..(3434)
; OTHER INFORMATION: BRCA2 repeat domain identified by Pfam, accession name
; OTHER INFORMATION: BRCA2_repeat, E-value=3.1e-166, Pfam score of 565.7
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(4766)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-273-573-8539

Query Match 57.4%; Score 31; DB 6; Length 4766;
Best Local Similarity 55.6%; Pred. No. 6.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EYLVPQOGF 10
|:|: |:|
Db 1071 EHLISQKGF 1079

Search completed: July 28, 2003, 17:14:00
Job time : 13 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2003, 16:45:39 ; Search time 22 Seconds
(without alignments)
21.376 Million cell updates/sec

Title: US-09-930-125-3
Perfect score: 54
Sequence: 1 EBYLPQGGF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match, 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	245	1 ERB2_MOUSE	P70424 mus musculus
2	54	100.0	1254	1 ERB2_MESAU	Q60553 mesocricetu
3	54	100.0	1255	1 ERB2_HUMAN	P04626 homo sapien
4	54	100.0	1257	1 ERB2_RAT	P08494 rattus norv
5	50	92.6	1210	1 EGFR_HUMAN	P00533 homo sapien
6	50	92.6	1210	1 EGFR_MOUSE	Q01279 mus musculus
7	46	85.2	540	1 ERBB_AVIEU	P11273 avian eryth
8	46	85.2	604	1 ERBB_AVIER	P00535 avian eryth
9	46	85.2	634	1 ERBB_ALV	P00534 avian leuko
10	38	70.4	232	1 YH73_SYNY3	P73623 synchocyst
11	37	68.5	95	1 ERB4_MOUSE	Q61527 mus musculus
12	37	68.5	687	1 TGM2_BOVIN	P51176 bos taurus
13	37	68.5	687	1 TGM2_HUMAN	P21980 homo sapien
14	37	68.5	689	1 TGM2_CAVCU	P08587 cavia cutie
15	37	68.5	1308	1 ERB4_HUMAN	Q15303 homo sapien
16	37	68.5	1308	1 ERB4_RAT	Q62956 rattus norv
17	36	66.7	541	1 FTCD_HUMAN	Q95954 h formimido
18	35	64.8	391	1 CAJ1_YEAST	P39101 saccharomyc
19	35	64.8	686	1 TGM2_MOUSE	P21981 mus musculus
20	35	64.8	917	1 NTA2_ARATH	P1035 arabidopsis
21	35	64.8	1242	1 MSB6_YEAST	Q03834 saccharomyc
22	35	64.8	2269	1 WRG9_HUMAN	Q90516 homo sapien
23	34	63.0	262	1 YF59_HELPJ	Q92190 helicobacte
24	34	63.0	364	1 MURG_THETN	Q82996 thermoaer
25	34	63.0	365	1 MURG_SHEVI	Q9FIN0 shewanella
26	34	63.0	474	1 SYE_BUCAP	Q8KA47 buchnera ap
27	34	63.0	541	1 FTCD_PIG	P53603 s formimido
28	34	63.0	598	1 NUSM1_PETWA	Q35543 petromyzon
29	34	63.0	988	1 TNP2_ECOLI	P06694 escherichia
30	34	63.0	997	1 Y114_MYCPN	P75183 mycoplasma
31	34	63.0	1097	1 TOLL_DROME	P08953 drosophila
32	34	63.0	1290	1 POLG_EMCV	P03304 encephalomy
33	34	63.0	2292	1 POLG_EMCVB	P17593 encephalomy

34	34	63.0	2292	1	POLG_EMCVB
35	33	61.1	262	1	YE59_HELPY
36	33	61.1	370	1	MYOM_APLCA
37	33	61.1	390	1	NCF1_MOUSE
38	33	61.1	392	1	YAV1_SCHPO
39	33	61.1	439	1	LIP1_DROME
40	33	61.1	459	1	T7L2_MOUSE
41	33	61.1	541	1	FTCD_MOUSE
42	33	61.1	541	1	FTCD_RAT
43	33	61.1	584	1	T7L1_MOUSE
44	33	61.1	588	1	T7L1_HUMAN
45	33	61.1	619	1	T7L2_HUMAN

ALIGNMENTS

RESULT 1
ERB2_MOUSE
ID ERB2_MOUSE STANDARD; PRT; 245 AA.
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Receptor protein-tyrosine kinase erbB-2 (EC 2.7.1.112) (p185erbB2)
DE (NEU proto-oncogene) (C-erbB-2) (Fragments).
GN ERBB2 OR NEU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-149 FROM N.A.
RC STRAIN=CD-1; TISSUE=Uterus;
RX MEDLINE=97200814; PubMed=9048643;
RA Lim J., Dey S.K., Das S.K.;
RT "Differential expression of the erbB2 gene in the perimplantation mouse uterus: potential mediator of signaling by epidermal growth factor-like growth factors";
RT Endocrinology 138:1328-1337(1997).
RL [2]
RN [2]
RP SEQUENCE OF 150-245 FROM N.A.
RX MEDLINE=96069911; PubMed=7589796;
RA Moscoso L.M., Chu G.C., Gautam M., Noakes P.G., Merlie J.P., Sanes J.R.;
RT "Synapse-associated expression of an acetylcholine receptor-inducing protein, ARIA/heretulin, and its putative receptors, ErbB2 and ErbB3, in developing mammalian muscle";
RT Dev. Biol. 172:158-169(1995).
RL [3]
RN [3]
RP INTERACTION WITH PRKCABP.
RX MEDLINE=21226773; PubMed=11278603;
RA Jaulin-Bastard F., Saito H., Le Bivic A., Ollendorff V., Marchetto S., Birnbaum D., Borg J.-P.;
RT "The ERBB2/HER2 receptor differentially interacts with ERBIN and PICK1 PSD-95/DLG/ZO-1 domain proteins";
RL J. Biol. Chem. 276:15256-15263(2001).
CC -1- FUNCTION: Essential component of a neuroligin-receptor complex, although neuroligins do not interact with it alone. GR30 is a potential ligand for this receptor. Not activated by EGF, TGF-alpha and amphiregulin.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
CC -1- SUBUNIT: Heterodimer with each of the other ERBB receptors (Potential). Interacts with PRKCABP.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed predominantly in uterine epithelial cells. In the muscle, expression localizes to the synaptic sites of muscle fibers.
CC -1- DEVELOPMENTAL STAGE: On days 1-4 of pregnancy, ERBB2 is detected primarily in epithelial cells, the day 1 uterus showing the highest accumulation. On day 5, the epithelium and the decidualizing stromal cells around the implanting blastocyst

exhibit accumulation of this receptor. On days 6-8, the expression persists in the epithelium at both the implantation and interimplantation sites in addition to modest levels in the secondary decidua zone. On days 7 and 8, accumulation is also prominent in the trophoblastic giant cells.

-1- PFM: Ligand-binding increases phosphorylation on tyrosine residues (By similarity).

-1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.

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EMBL; U71126; AAB17380.1; -
 EMBL; L47239; AAA93532.1; -
 DR HSSP; P11362; IFGK.
 DR MGD; MGI:95410; Erbb2.
 DR GO; GO:0007507; P:heart development; IMP.
 DR GO; GO:0007422; P:peripheral nervous system development; IMP.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; PARTIAL.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 KW Transmembrane; Glycoprotein; Multigene family; Receptor; Transferase;
 KW Tyrosine-protein kinase; ATP-binding; Phosphorylation.
 FT NON_TER 1 1
 FT DOMAIN <1 >149 PROTEIN KINASE.
 FT ACT_SITE 61 61 BY SIMILARITY.
 FT NON_CONS 149 150
 FT NON_TER 245 245
 SQ SEQUENCE 245 AA; 26927 MW; 0F763F0363DPEFIC CRC64;

Query Match 100.0%; Score 54; DB 1; Length 245;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEYLVPPQGF 10
 |||||
 Db 160 EEYLVPPQGF 169

RESULT 2
 ERB2_MESAU
 ID ERB2_MESAU STANDARD; PRT; 1254 AA.
 AC Q60553;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112)
 DE (p185erbB2) (NEU proto-oncogene) (C-erbB-2).
 GN ERB2 OR NEU.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Nerve;
 RX MEDLINE=94193007; PubMed=7908275;
 RA Nakamura T., Ushijima T., Ishizaka Y., Nagao M., Arai M.,
 RA Yamazaki Y., Ishikawa T.;
 RT "Cloning and activation of the Syrian hamster neu proto-oncogene."
 RT Gene 140:251-255(1994).
 CC -1- FUNCTION: Essential component of a neuroregulin-receptor complex,
 CC although neuroregulins do not interact with it alone. GP30 is a

potential ligand for this receptor. Not activated by EGF, TGF-alpha and amphiregulin (By similarity).

-1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein tyrosine phosphate.

-1- SUBUNIT: Heterodimer with each of the other ERBB receptors (Potential). Interacts with PRKCA/BP (By similarity).

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- PFM: Ligand-binding increases phosphorylation on tyrosine residues.

-1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.

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EMBL; D16295; BAA03801.1; -
 DR PIR; I48161; I48161.
 DR HSSP; P11362; IFGK.
 DR InterPro; IPR000494; EGFR_L_domain.
 DR InterPro; IPR006211; Furin-like.
 DR InterPro; IPR006212; Furin-repeat.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR004019; YLP_motif.
 DR Pfam; PF00757; Furin-like; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF01030; Recep_L_domain; 2.
 DR Pfam; PF02757; YLP; 2.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Prot_kinase; 1.
 DR SMART; SM00261; FU; 4.
 DR SMART; SM00219; TyrcK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 KW Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
 KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Proto-oncogene; Disease mutation.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 1254 RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2.
 FT DOMAIN 22 652 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 653 675 POTENTIAL.
 FT DOMAIN 676 1254 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 158 368 CYS-RICH.
 FT DOMAIN 720 987 CYS-RICH.
 FT NP_BIND 726 734 PROTEIN KINASE.
 FT BINDING 753 753 ATP (BY SIMILARITY).
 FT ACT_SITE 845 845 ATP (BY SIMILARITY).
 FT DISULFID 195 204 BY SIMILARITY.
 FT DISULFID 199 212 BY SIMILARITY.
 FT DISULFID 236 244 BY SIMILARITY.
 FT DISULFID 240 252 BY SIMILARITY.
 FT DISULFID 255 264 BY SIMILARITY.
 FT DISULFID 268 295 BY SIMILARITY.
 FT DISULFID 299 311 BY SIMILARITY.
 FT DISULFID 315 331 BY SIMILARITY.
 FT DISULFID 334 338 BY SIMILARITY.
 FT DISULFID 511 520 BY SIMILARITY.
 FT DISULFID 515 528 BY SIMILARITY.
 FT DISULFID 531 540 BY SIMILARITY.
 FT DISULFID 544 560 BY SIMILARITY.
 FT DISULFID 563 576 BY SIMILARITY.
 FT DISULFID 584 596 BY SIMILARITY.
 FT DISULFID 587 596 BY SIMILARITY.
 FT DISULFID 600 623 BY SIMILARITY.
 FT DISULFID 626 634 BY SIMILARITY.
 FT DISULFID 630 642 BY SIMILARITY.
 MOD_RES 1139 1139 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

FT MOD_RES 1247 1247 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 68 68 N-LINKED (GLCNAC) (POTENTIAL).
 FT CARBOHYD 125 125 N-LINKED (GLCNAC) (POTENTIAL).
 FT CARBOHYD 187 187 N-LINKED (GLCNAC) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAC) (POTENTIAL).
 FT CARBOHYD 530 530 N-LINKED (GLCNAC) (POTENTIAL).
 FT CARBOHYD 571 571 N-LINKED (GLCNAC) (POTENTIAL).
 FT CARBOHYD 629 629 N-LINKED (GLCNAC) (POTENTIAL).
 FT VARIANT 658 658 V -> E (IN ONCOGENIC NEU).
 FT VARIANT 659 659 V -> E (IN ONCOGENIC NEU).
 SQ SEQUENCE 1254 AA; 138252 MW; 974C3791C21F2BE1 CRC64;
 Query Match 100.0%; Score 54; DB 1; Length 1254;
 Best Local Similarity 100.0%; Pred. No. 0.011; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EYLVPQOGF 10
 Db 1021 EYLVPQOGF 1030
 RESULT 3
 ID ERB2_HUMAN STANDARD; PRT; 1255 AA.
 AC P04626;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DE Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112)
 DE (p185erbB2) (NEU proto-oncogene) (C-erbB-2) (Tyrosine kinase-type cell
 DE surface receptor HER2) (MLN 19).
 GN ERBB2 OR HER2 OR NGL OR NEU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86118663; PubMed=3003577;
 RA Yamamoto T., Ikawa S., Akiyama T., Semba K., Nomura N., Miyajima N.,
 RA Saito T., Toyoshima K.;
 RT "Similarity of protein encoded by the human c-erb-B-2 gene to
 RT epidermal growth factor receptor.";
 RL Nature 319:230-234(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86070181; PubMed=2999974;
 RA Coussens L., Yang-Feng T.L., Liao Y.C., Chen E., Gray A.,
 RA McGrath J., Seeburg P.H., Libermann T.A., Schlessinger J.,
 RA Francke U., Levinson A., Ullrich A.;
 RT "Tyrosine kinase receptor with extensive homology to EGF receptor
 RT shares chromosomal location with neu oncogene.";
 RL Science 230:1132-1139(1985).
 RN [3]
 RP SEQUENCE OF 737-1031 FROM N.A.
 RX MEDLINE=86016729; PubMed=2995967;
 RA Semba K., Kanata N., Toyoshima K., Yamamoto T.;
 RT "A v-erbB-related protooncogene, c-erbB-2, is distinct from the
 RT c-erbB-1/epidermal growth factor-receptor gene and is amplified in a
 RT human salivary gland adenocarcinoma.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:6497-6501(1985).
 RN [4]
 RP VARIANTS VAL-654 AND VAL-655.
 RX MEDLINE=93194196; PubMed=8095486;
 RA Ehsani A., Low J., Wallace R.B., Wu A.M.;
 RT "Characterization of a new allele of the human ERBB2 gene by allele-
 RT specific competition hybridization.";
 RL Genomics 15:426-429(1993).
 CC -1- FUNCTION: Essential component of a neuroligin-receptor complex,
 CC although neuroligins do not interact with it alone. GP30 is a
 CC potential ligand for this receptor. Not activated by EGF, TGF-
 CC alpha and amphiregulin.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein

CC tyrosine phosphate.
 CC -1- SUBUNIT: Heterodimer with each of the other ERBB receptors
 CC (POTENTIAL). Interacts with PRKCAP (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- PTM: Ligand-binding increases phosphorylation on tyrosine
 CC residues (By similarity).
 CC -1- POLYMORPHISM: There are four alleles due to the variations in
 CC positions 654 and 655. Allele B1 (654-Ile-Ile-655) has a frequency
 CC of 0.782; allele B2 (654-Ile-Val-655) has a frequency of 0.206;
 CC allele B3 (654-Val-Val-655) has a frequency of 0.012.
 CC -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC
 CC -----
 CC EMBL; M11767; AAA35808.1; JOINED.
 CC EMBL; M11761; AAA35808.1; JOINED.
 CC EMBL; M11762; AAA35808.1; JOINED.
 CC EMBL; M11763; AAA35808.1; JOINED.
 CC EMBL; M11764; AAA35808.1; JOINED.
 CC EMBL; M11765; AAA35808.1; JOINED.
 CC EMBL; M11766; AAA35808.1; JOINED.
 CC EMBL; M11730; AAA75493.1; JOINED.
 CC EMBL; M12036; AAA35978.1; JOINED.
 CC EMBL; X03363; CAA27060.1; JOINED.
 CC PIR; A24571; A24571.
 CC PDB; 1N82; 18-FEB-03.
 CC PDB; 1QRI; 01-JAN-00.
 CC Gene; HGNC:3430; ERBB2.
 CC MIM; 164870; .
 CC GO; GO:0005012; F:Neu/ErbB-2 receptor activity; TAS.
 CC GO; GO:0004716; F:receptor signaling protein tyrosine kinase . . . TAS.
 CC GO; GO:0008283; P:cell proliferation; TAS.
 CC GO; GO:0007048; P:oncogenesis; TAS.
 CC GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
 CC GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
 CC InterPro; IPR000494; EGFR_L_domain.
 CC InterPro; IPR006211; Furin-like.
 CC InterPro; IPR006212; Furin-repeat.
 CC InterPro; IPR00719; Prot_kinase.
 CC InterPro; IPR001245; Tyr_kinase.
 CC InterPro; IPR004019; YLP_motif.
 CC Pfam; PF00757; Furin-like; 1.
 CC Pfam; PF00069; pkinase; 1.
 CC Pfam; PF01030; Recep_L_domain; 2.
 CC Pfam; PF02757; YLP; 2.
 CC PRINTS; PD000001; Prot_kinase; 1.
 CC ProDom; PD000001; Prot_kinase; 1.
 CC SMART; SM00261; FU; 4.
 CC SMART; SM00219; Tyrc; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 CC Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
 CC Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 CC Polymorphism; 3D-structure.
 CC SIGNAL 1 21
 CC CHAIN 22 1255
 CC DOMAIN 22 652
 CC TRANSMEM 653 675
 CC DOMAIN 676 1255
 CC DOMAIN 720 987
 CC NP_BIND 726 734
 CC BINDING 753 753
 CC ACT_SITE 845 845
 CC DISULFID 195 204
 CC DISULFID 199 212
 CC DISULFID 220 227


```
FT DISULFID 224 235 BY SIMILARITY.
FT DISULFID 236 244 BY SIMILARITY.
FT DISULFID 240 252 BY SIMILARITY.
FT DISULFID 255 264 BY SIMILARITY.
FT DISULFID 268 295 BY SIMILARITY.
FT DISULFID 311 331 BY SIMILARITY.
FT DISULFID 334 338 BY SIMILARITY.
FT DISULFID 511 520 BY SIMILARITY.
FT DISULFID 515 528 BY SIMILARITY.
FT DISULFID 531 540 BY SIMILARITY.
FT DISULFID 544 560 BY SIMILARITY.
FT DISULFID 563 576 BY SIMILARITY.
FT DISULFID 567 584 BY SIMILARITY.
FT DISULFID 587 596 BY SIMILARITY.
FT DISULFID 600 623 BY SIMILARITY.
FT DISULFID 626 634 BY SIMILARITY.
FT DISULFID 630 642 BY SIMILARITY.
FT MOD_RES 1139 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 1248 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 530 530 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 654 654 I -> V (IN dBSNP:1801201).
FT VARIANT 655 655 /FTID-VAR_004077.
FT VARIANT 1170 1170 I -> V (IN dBSNP:1801200).
FT CONFLICT 1170 1170 P -> A (IN REF. 2).
FT SEQUENCE 1255 AA; 137909 MW; 39E9DFDA04DCF962 CRC64;

Query Match 100.08; Score 54; DB 1; Length 1255;
Best Local Similarity 100.08; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBYLVPOQGF 10
Db 1021 EBYLVPOQGF 1030

RESULT 4
ERB2_RAT STANDARD; PRT; 1257 AA.
ID P06494;
DC 01-JAN-1988 (Rel. 06, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112)
DE (p185erbB2) (NEU proto-oncogene) (C-erbB-2) (Epidermal growth factor
DE receptor-related protein).
GN ERB2 OR NEU.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Neuroblastoma;
RX MEDLINE=86118662; PubMed=3945311;
RA Bargmann C.I., Hung M.-C., Weinberg R.A.;
RT "The new oncogene encodes an epidermal growth factor receptor-related
RL protein.";
RL Nature 319:226-230(1986).
RN [2]
RP SEQUENCE OF 852-905 FROM N.A.
RC TISSUE=Sciatic nerve;
RX MEDLINE=91222560; PubMed=2025425;
RA Lai C., Lemke G.;
RT "An extended family of protein-tyrosine kinase genes differentially
RT expressed in the vertebrate nervous system.";
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Neuron 6:691-704(1991).
[3]
RN STRUCTURE BY NMR OF 650-668.
RX MEDLINE=92155181; PubMed=1346763;
RA Gullick W.J., Bottomley A.C., Loftis F.J., Doak D.G., Mulvey D.,
RA Newman R., Crumpton M.J., Sternberg M.J.E., Campbell I.D.;
RT "Three dimensional structure of the transmembrane region of the proto-
RL oncogenic and oncogenic forms of the neu protein.";
RL EMBO J. 11:43-48(1992).
CC -1- FUNCTION: Essential component of a neuroregulin-receptor complex,
CC although neuroregulins do not interact with it alone. GP30 is a
CC potential ligand for this receptor. Not activated by EGF, TGF-
CC alpha and amphiregulin.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: Heterodimer with each of the other ERBB receptors. The
CC constitutively activated oncogenic variant forms a homodimer.
CC Interacts with PRKCAP (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- PTM: Ligand-binding increases phosphorylation on tyrosine
CC residues (By similarity).
CC -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X03362; CAA27059.1; ALT_INIT.
CC PDB: 1IJJ; 27-JUN-01.
CC InterPro: IPR000494; EGFR_L_domain.
CC InterPro: IPR006211; Furin-like.
CC InterPro: IPR006212; Furin_repeat.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR001245; Tyr_pkinase.
CC InterPro: IPR004019; YLP_motif.
CC Pfam: PF00757; Furin-like; 1.
CC Pfam: PF00069; pkinase; 1.
CC Pfam: PF01030; Recep_L_domain; 2.
CC Pfam: PF02757; YLP; 2.
CC PRINTS: PR00109; TYRKINASE.
CC PRODOM: PD000001; Prot_kinase; 1.
CC SMART: SM00261; FU; 4.
CC SMART: SM00219; TyrKc; 1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
CC Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
CC Proto-oncogene; Disease mutation; 3D-structure.
CC SIGNAL 1 21
CC CHAIN 22 1257 RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2.
CC DOMAIN 22 654 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 655 677 POTENTIAL.
CC DOMAIN 678 1257 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 159 369 CYS-RICH.
CC DOMAIN 473 646 CYS-RICH.
CC DOMAIN 722 989 PROTEIN KINASE.
CC NP_BIND 728 736 ATP (BY SIMILARITY).
CC BINDING 755 755 ATP (BY SIMILARITY).
CC ACT_SITE 847 847 BY SIMILARITY.
CC DISULFID 196 205 BY SIMILARITY.
CC DISULFID 200 213 BY SIMILARITY.
CC DISULFID 221 228 BY SIMILARITY.
CC DISULFID 225 236 BY SIMILARITY.
CC DISULFID 237 245 BY SIMILARITY.
CC DISULFID 241 253 BY SIMILARITY.
CC DISULFID 256 265 BY SIMILARITY.
CC DISULFID 269 296 BY SIMILARITY.
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FT DISULFID 300 312 BY SIMILARITY.
FT DISULFID 316 332 BY SIMILARITY.
FT DISULFID 335 339 BY SIMILARITY.
FT DISULFID 513 522 BY SIMILARITY.
FT DISULFID 517 530 BY SIMILARITY.
FT DISULFID 533 542 BY SIMILARITY.
FT DISULFID 546 562 BY SIMILARITY.
FT DISULFID 565 578 BY SIMILARITY.
FT DISULFID 569 586 BY SIMILARITY.
FT DISULFID 589 598 BY SIMILARITY.
FT DISULFID 602 625 BY SIMILARITY.
FT DISULFID 628 636 BY SIMILARITY.
FT DISULFID 632 644 BY SIMILARITY.
FT MOD_RES 1141 1250 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 1250 1250 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 532 532 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 573 573 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 631 631 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 661 661 V -> E (IN ONCOGENIC NEU).
SQ SEQUENCE 1257 AA; 138831 MW; 6129264583011402 CRC64;

Query Match 100.0%; Score 54; DB 1; Length 1257;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEVLVPOQGF 10
Db 1023 EEVLVPOQGF 1032

RESULT 5
EGFR_HUMAN STANDARD; PRT; 1210 AA.
AC P00533; O00688; Q00732; P06268; Q14225; Q92795; Q9B252; Q9GEX1;
AC Q9H2C9; Q9H3C9; Q9UMD7; Q9UMDB; Q9UMG5;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Epidermal growth factor receptor precursor (EC 2.7.1.112) (Receptor
DE protein-tyrosine kinase ErbB-1).
GN EGFR OR ERBB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=84219729; PubMed=6328312;
RA Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Tam A.W.,
RA Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J.,
RA Mayes E.L.V., Whittle N., Waterfield M.D., Saeburg P.H.;
RA "Human epidermal growth factor receptor cDNA sequence and aberrant
RT expression of the amplified gene in A431 epidermoid carcinoma cells.";
RL Nature 309:418-425(1984).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=84219729; PubMed=6328312;
RA Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Tam A.W.,
RA Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J.,
RA Mayes E.L.V., Whittle N., Waterfield M.D., Saeburg P.H.;
RA "Human epidermal growth factor receptor cDNA sequence and aberrant
RT expression of the amplified gene in A431 epidermoid carcinoma cells.";
RL Nature 309:418-425(1984).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=95382957; PubMed=7654368;
RA Ilekis J.V., Stark B.C., Scoccia B.;
RA "Possible role of variant RNA transcripts in the regulation of
RT epidermal growth factor receptor expression in human placenta.";
RL Mol. Reprod. Dev. 41:149-156(1995).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=97078686; PubMed=8918811;
RA Reiter J.L., Maible N.J.;
RA "A 1.8 kb alternative transcript from the human epidermal growth
RT factor receptor gene encodes a truncated form of the receptor.";
RL Nucleic Acids Res. 24:4050-4056(1996).

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RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=9725647; PubMed=9103388;
RA Ilekis J.V., Gariti J., Niederberger C., Scoccia B.;
RA "Expression of a truncated epidermal growth factor receptor-like
RT protein (TEGFR) in ovarian cancer.";
RL Gynecol. Oncol. 65:36-41(1997).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).
RX MEDLINE=21100872; PubMed=11161793;
RA Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
RA Schehl Sinclair C., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
RA Balasubramaniam S., Crossley T.D., Magnuson T.R., James C.D.,
RA Maible N.J.;
RA "Comparative genomic sequence analysis and isolation of human and
RT mouse alternative EGFR transcripts encoding truncated receptor
RT isoforms.";
RL Genomics 71:1-20(2001).
RN [6]
RP SEQUENCE OF 575-687 FROM N.A.
RA Reiter J.L., Threadgill D.W., Danielsen A.J., Schehl C.M.,
RA Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R.,
RA Maible N.J.;
RA "Human and mouse alternative EGFR transcripts encoding only the
RT extracellular domain of the receptor.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE OF 713-924 FROM N.A.
RX MEDLINE=84196372; PubMed=6326261;
RA Lin C.R., Chen W.S., Krueger W., Stolarsky L.S., Weber W.,
RA Evans R.M., Verma I.M., Gill G.N., Rosenfeld M.G.;
RA "Expression cloning of human EGF receptor complementary DNA: gene
RT amplification and three related messenger RNA products in A431
RT cells.";
RL Science 224:843-848(1984).
RN [8]
RP SEQUENCE OF 150-962 FROM N.A.
RX MEDLINE=84245835; PubMed=6330563;
RA Xu Y.H., Ishii S., Clark A.J.L., Sullivan M., Wilson R.K., Ma D.P.,
RA Roe B.A., Merlino G.T., Pastan I.;
RA "Human epidermal growth factor receptor cDNA is homologous to a
RT variety of RNAs overproduced in A431 carcinoma cells.";
RL Nature 309:806-810(1984).
RN [9]
RP SEQUENCE OF 1028-1210 FROM N.A.
RX MEDLINE=85046483; PubMed=6093780;
RA Simmen F.A., Gope M.L., Schulz T.Z., Wright D.A., Carpenter G.,
RA O'Malley B.W.;
RA "Isolation of an evolutionarily conserved epidermal growth factor
RT receptor cDNA from human A431 carcinoma cells.";
RL Biochem. Biophys. Res. Commun. 124:125-132(1984).
RN [10]
RP SEQUENCE OF 1-29 FROM N.A.
RX MEDLINE=86217333; PubMed=3329716;
RA Haley J.D., Whittle N., Bennett P., Kinchington D., Ullrich A.,
RA Waterfield M.D.;
RA "The human EGF receptor gene: structure of the 110 kb locus and
RT identification of sequences regulating its transcription.";
RL Oncogene Res. 1:375-396(1987).
RN [11]
RP SEQUENCE OF 1-29 FROM N.A.
RX MEDLINE=91107677; PubMed=1988448;
RA Haley J.D., Waterfield M.D.;
RA "Contributory effects of de novo transcription and premature
RT transcript termination in the regulation of human epidermal growth
RT factor receptor proto-oncogene RNA synthesis.";
RL J. Biol. Chem. 266:1746-1753(1991).
RN [12]
RP SEQUENCE OF 1-29 FROM N.A.
RX MEDLINE=85270438; PubMed=2991899;
RA Ishii S., Xu Y.H., Stratton R.H., Roe B.A., Merlino G.T., Pastan I.;

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RT "Characterization and sequence of the promoter region of the human.
 RL epidermal growth factor receptor gene.";
 RN Proc. Natl. Acad. Sci. U.S.A. 82:4920-4924(1985).
 RP SEQUENCE OF 540.
 RA Kohda D.;
 RL Submitted (SEP-1997) to the SWISS-PROT data bank.
 RP RECEPTOR ACTIVITY.
 RX MEDLINE=84191554; PubMed=6325948;
 RA Mroczkowski B., Mosig G., Cohen S.;
 RT "ATP-stimulated interaction between epidermal growth factor receptor
 RL and supercoiled DNA.";
 RL Nature 309:270-273(1984).
 RP PHOSPHORYLATION.
 RX MEDLINE=89278137; PubMed=2543678;
 RA Margolis B.L., Lax I., Kris R., Dombalagian M., Honegger A.M.,
 RA Hawk R., Givol D., Ullrich A., Schlessinger J.;
 RT "All autophosphorylation sites of epidermal growth factor (EGF)
 RL receptor and HER2/neu are located in their carboxyl-terminal tails.
 RL Identification of a novel site in EGF receptor.";
 RL J. Biol. Chem. 264:10667-10671(1989).
 RP CARBOHYDRATE-LINKAGE SITES ASN-128; ASN-175; ASN-413; ASN-444 AND
 RP ASN-528.
 RX MEDLINE=96398132; PubMed=8962717;
 RA Smith K.D., Davies M.J., Bailey D., Renouf D.V., Hounsell E.F.;
 RT "Analysis of the glycosylation patterns of the extracellular domain of
 RL the epidermal growth factor receptor expressed in Chinese hamster
 RL ovary fibroblasts.";
 RL Growth Factors 13:121-132(1996).
 RP CARBOHYDRATE-LINKAGE SITES ASN-56; ASN-352; ASN-361; ASN-568 AND
 RP ASN-603.
 RX MEDLINE=20198209; PubMed=10731668;
 RA Sato C., Kim J.-H., Abe Y., Saito K., Yokoyama S., Kohda D.;
 RT "Characterization of the N-oligosaccharides attached to the atypical
 RL Asn-X-Cys sequence of recombinant human epidermal growth factor
 RL receptor.";
 RL J. Biol. Chem. 273:11150-11157(1998).
 RP REVIEW.
 RX MEDLINE=87297456; PubMed=3039909;
 RA Carpenter G.;
 RT "Receptors for epidermal growth factor and other polypeptide
 RL mitogens.";
 RL Annu. Rev. Biochem. 56:881-914(1987).
 RP INTERACTION WITH RIPK1.
 RX PubMed=11116146;
 RA Habib A.A., Chatterjee S., Park S.-K., Ratan R.R., Lefebvre S.,
 RA Vartanian T.;
 RT "The epidermal growth factor receptor engages receptor interacting
 RL protein and nuclear factor-kappa B (NF-kappa B)-inducing kinase to
 RL activate NF-kappa B. Identification of a novel receptor-tyrosine
 RL kinase signalosome.";
 RL J. Biol. Chem. 276:8865-8874(2001).
 CC -!- FUNCTION: Receptor for EGF, but also for other members of the EGF
 CC family, as TGF-alpha, amphiregulin, betacellulin, heparin-binding
 CC EGF-like growth factor, Gp30 and vaccinia virus growth factor. Is
 CC involved in the control of cell growth and differentiation.
 CC -!- FUNCTION: Isoform 2/truncated isoform may act as an antagonist.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBUNIT: Binds RIPK1.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Isoform 2 is

CC secreted
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=4;
 CC Name=1; Synonyms=pi170;
 CC IsoId=P00533-1; Sequence=Displayed;
 CC Name=2; Synonyms=pe60, Truncated, TEGFR;
 CC IsoId=P00533-2; Sequence=VSP_002887, VSP_002888;
 CC Name=3; Synonyms=pi110;
 CC IsoId=P00533-3; Sequence=VSP_002889, VSP_002890;
 CC Name=4;
 CC IsoId=P00533-4; Sequence=VSP_002891, VSP_002892;
 CC -!- TISSUE SPECIFICITY: Expressed in placenta. Isoform 2 is also
 CC expressed in ovarian cancers.
 CC -!- MISCELLANEOUS: Binding of EGF to the receptor leads to
 CC dimerization, internalization of the EGF-receptor complex,
 CC induction of the tyrosine kinase activity, stimulation of cell DNA
 CC Query Match 92.6%; Score 50; DB 1; Length 1210;
 CC Best Local Similarity 80.0%; Pred. No. 0.066;
 CC Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EYLVPPQGF 10
 Db 1014 DEVLIPQGF 1023
 RESULT 6
 EGF_MOUSE
 ID EGF_MOUSE STANDARD; PRT; 1210 AA.
 AC Q01279;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Epidermal growth factor receptor precursor (EC 2.7.1.112).
 GN EGF.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=93026370; PubMed=1408137;
 RA Avivi A., Skorecki K., Yayon A., Givol D.;
 RT "Promoter region of the murine fibroblast growth factor receptor 2
 RL (bek/KGFR) gene.";
 RL Oncogene 7:1957-1962(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c, and CD-1; TISSUE=Decidua, and Liver;
 RX MEDLINE=93126380; PubMed=7678348;
 RA Paria B.C., Das S.K., Andrews G.K., Dey S.K.;
 RT "Expression of the epidermal growth factor receptor gene is regulated
 RL in mouse blastocysts during delayed implantation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RA Hibbs M.L.;
 RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6/C3; TISSUE=Liver;
 RX MEDLINE=94170986; PubMed=8125255;
 RA Luetke N.C., Phillips H.K., Qiu T.H., Copeland N.G., Earp H.S.,
 RA Jenkins N.A., Lee D.C.;
 RT "The mouse waved-2 phenotype results from a point mutation in the EGF
 RL receptor tyrosine kinase.";
 RL Genes Dev. 8:399-413(1994).
 RN [5]
 RP SEQUENCE OF 1-714 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=91232866; PubMed=2030916;

RA Avivi A., Lax I., Ullrich A., Schlessinger J., Givol D., Morse B.:
 RT "Comparison of EGF receptor sequences as a guide to study the ligand
 RL binding site.";
 RN Oncogene 6:673-676(1991).
 [6]
 RP SEQUENCE OF 969-1117 FROM N.A.
 RC STRAIN-C3H;
 RA Eisinger D.P., Serrero G.;
 RL Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF,
 CC AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP30 AND
 CC VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: Binds RPK1 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- MISCELLANEOUS: Binding of EGF to the receptor leads to
 CC dimerization, internalization of the EGF-receptor complex,
 CC induction of the tyrosine kinase activity, stimulation of cell DNA
 CC synthesis, and cell proliferation.
 CC -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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 CC -----
 DR EMBL; X78987; CAA55587.1; -;
 DR EMBL; U03425; AAA17899.1; -;
 DR EMBL; X59698; CAA42219.1; -;
 DR EMBL; L06864; AAA53029.1; -;
 DR EMBL; Z12608; CAA78249.1; -;
 DR PIR; A53183; A53183.
 DR HSP; P11362; IFGK.
 DR MG; MG1.95294; Egrf.
 DR GO; GO:0030139; C:endocytic vesicle; IDA.
 DR GO; GO:0005622; C:intracellular; IDA.
 DR InterPro; IPR000494; EGFR_L_domain.
 DR InterPro; IPR006211; Furin-like.
 DR InterPro; IPR006212; Furin_repeat.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00757; Furin-like; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF01030; Recep_L_domain; 2.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Prot_kinase; 1.
 DR SMART; SM00261; FU; 5.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR Transmembrane; Glycoprotein; Receptor; Signal; Transferase;
 KW Tyrosine-protein kinase; ATP-binding; phosphorylation; Repeat.
 FT SIGNAL 1 24
 FT CHAIN 25 1210
 FT DOMAIN 25 647
 FT TRANSMEM 648 670
 FT DOMAIN 671 1210
 FT REPEAT 75 300
 FT REPEAT 390 600
 FT DOMAIN 1028 1071
 FT DOMAIN 714 981
 FT NP_BIND 720 728
 FT BINDING 747 747
 FT ACT_SITE 839 839
 FT DISULFID 190 199
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 FT DISULFID 215 223
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 FT DISULFID 624 636
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 FT MOD_RES 1110 1110
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 FT CARBOHYD 623 623
 FT CONFLICT 19 19
 FT CONFLICT 539 539
 FT CONFLICT 991 991
 FT CONFLICT 1116 1117
 FT CONFLICT 1210 1210
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 Query Match 92.6%; Score 50; DB 1; Length 1210;
 Best Local Similarity 80.0%; Pred. No. 0.066;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 BEYLPVQGGF 10
 :||||:|||||
 Db 1016 DEYLPVQGGF 1025
 RESULT 7
 ID ERBB_AVIEU STANDARD; PRT; 540 AA.
 AC P11273;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase transforming protein erbB (BC 2.7.1.112).
 GN V-ERBB.
 OS Avian erythroblastosis virus (strain ts167).
 OC Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
 OX NCBI_TaxID=103898;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87064458; PubMed=2878364;
 RA Choi O.R., Trainor C., Graf T., Beug H., Engel J.D.;
 RT "A single amino acid substitution in v-erbB confers a thermolabile
 RT phenotype to ts167 avian erythroblastosis virus-transformed erythroid
 RT cells.";
 RL Mol. Cell. Biol. 6:1751-1759(1986).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
 CC -----
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CC EMBL; M13179; AAA42401.1; -
 DR PIR; A25231; TVFVEB.
 DR HSP; P11362; IFGK.
 DR InterPro; IPR000719; Prot_Kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_Kinase; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Tyrosine-protein kinase; ATP-binding; Oncogene;
 KW Glycoprotein; Phosphorylation.
 FT DOMAIN 132 399
 FT NP_BIND 138 146 ATP (BY SIMILARITY).
 FT BINDING 165 165 ATP (BY SIMILARITY).
 FT ACT_SITE 257 257 BY SIMILARITY.
 FT VARIANT 270 270 H -> D (IN THERMOLABILE V-ERBB).
 SQ SEQUENCE 540 AA; 60412 MW; 5B53297AA068B65D CRC64;

Query Match 85.2%; Score 46; DB 1; Length 540;
 Best Local Similarity 80.0%; Pred. No. 0.19;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EEVLVPQOGF 10
 :||||| |||
 DB 434 DEYLVPHQGF 443

RESULT 8

ERBB_AVIER
 ID ERBB_AVIER STANDARD; PRT; 604 AA.
 AC P00535;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112).
 GN V-ERBB.
 OS Avian erythroblastosis virus (strain ES4).
 OC Viruses; Retroviral viruses; Retroviridae; Avian type C retroviruses.
 OX NCBI_TaxID=79685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H;
 RX MEDLINE=84026539; PubMed=6313229;
 RA Yamamoto T., Nishida T., Miyajima N., Kawai S., Ooi T., Toyoshima K.;
 RT "The erbB gene of avian erythroblastosis virus is a member of the src
 RT gene family.";
 RL Cell 35:71-78(1983).
 RN [2]
 RP SEQUENCE OF 1-152 FROM N.A.
 RX MEDLINE=84223957; PubMed=6328658;
 RA Debouire B., Henry C., Benalissa M., Biserte G., Claverie J.-M.,
 RA Saule S., Martin P., Stéhelin D.;
 RT "Sequencing the erbA gene of avian erythroblastosis virus reveals a
 RT new type of oncogene.";
 RL Science 224:1456-1459(1984).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 CC tyrosine phosphate.
 CC -!- DISEASE: THE V-ERBB ONCOGENE TRANSFORMS AVIAN FIBROBLASTS AND
 CC ERYTHROBLASTS IN CULTURE AND INDUCES SARCOMAS AND ERYTHROLEUKEMIAS
 CC IN CHICKENS.
 CC -!- MISCELLANEOUS: V-ERBB IS A TRUNCATED AND MUTATED VERSION OF THE
 CC RECEPTOR FOR EPIDERMAL GROWTH FACTOR.
 CC -!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.

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CC EMBL; K02006; AAA42394.1; ALT_INIT.
 DR EMBL; K01216; AAA42400.1; -
 DR PIR; A00644; TVYUH.
 DR HSP; P11362; IFGK.
 DR InterPro; IPR000719; Prot_Kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_Kinase; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

KW Transferase; Tyrosine-protein kinase; ATP-binding; Oncogene;
 KW Glycoprotein; Phosphorylation.
 FT DOMAIN 132 399
 FT NP_BIND 138 146 ATP (BY SIMILARITY).
 FT BINDING 165 165 ATP (BY SIMILARITY).
 FT ACT_SITE 257 257 BY SIMILARITY.
 FT CONFLICT 29 29 R -> W (IN REF. 2).
 FT CONFLICT 140 140 S -> F (IN REF. 2).
 FT CONFLICT 146 146 I -> V (IN REF. 2).
 SQ SEQUENCE 604 AA; 67633 MW; 76BECDD06745D609 CRC64;

Query Match 85.2%; Score 46; DB 1; Length 604;
 Best Local Similarity 80.0%; Pred. No. 0.21;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EEVLVPQOGF 10
 :||||| |||
 DB 434 DEYLVPHQGF 443

RESULT 9

ERBB_ALV
 ID ERBB_ALV STANDARD; PRT; 634 AA.
 AC P00534;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112).
 GN V-ERBB.
 OS Avian leukosis virus.
 OC Viruses; Retroviral viruses; Retroviridae; Alpharetrovirus.
 OX NCBI_TaxID=11864;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85228222; PubMed=2988784;
 RA Nilsen T.W., Maroney P.A., Goodwin R.G., Rottman F.M.,
 RA Crittenden L.B., Raines M.A., Kung H.-J.;
 RT "c-erbB activation in ALV-induced erythroblastosis: novel RNA
 RT processing and promoter insertion result in expression of an
 RT amino-truncated EGF receptor.";
 RL Cell 41:719-726(1985).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 CC tyrosine phosphate.
 CC -!- MISCELLANEOUS: THIS PROTEIN IS PRODUCED BY ERYTHROLEUKEMIA CELLS
 CC IN CHICKS WHICH HAVE BEEN INJECTED WITH THE AVIAN LEUKOSIS VIRUS
 CC AND SUBSEQUENTLY DEVELOP LEUKEMIA. THE LEUKEMIAS ARE INDUCED BY
 CC THE INSERTION OF RETROVIRAL PROMOTER ELEMENTS IN OR NEAR THE
 CC C-ERBB GENE, WHICH LEADS TO C-ERBB ACTIVATION.
 CC -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-ENV-ERBB
 CC PROTEIN.
 CC -!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M10066; AAA48763.1; ALT_INIT.
CC HSPF: P11362; IFGK.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR001245; Tyr_pkinase.
CC Pfam: PF00069; pkinase; 1.
CC PRINTS: PR00109; TYRKINASE.
CC ProDom: PD000001; Prot_kinase; 1.
CC SMART: SM00219; TyrRC; 1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
CC PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
CC Transferrase: Tyrosine-protein kinase; ATP-binding; Oncogene;
KW Glycoprotein; Phosphorylation.
FT DOMAIN 132 399
FT NP_BIND 138 146 ATP (BY SIMILARITY).
FT BINDING 165 165 ATP (BY SIMILARITY).
FT ACT_SITE 257 257 BY SIMILARITY.
FT SEQUENCE 634 AA; 70891 MW; E705E33A0BE01FCC CRC64;
Query Match 85.2%; Score 46; DB 1; Length 634;
Best Local Similarity 80.0%; Pred. No. 0.22;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 EYLVPPQGGF 10
DB 434 DEYLVPPHGGF 443
RESULT 10
YH73_SYNY3
ID YH73_SYNY3 STANDARD; PRT; 232 AA.
AC P73623;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein sll1773.
GN SLL1773.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=11148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kofani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugitani M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -!- SIMILARITY: BELONGS TO THE PIRIN FAMILY.
CC -----
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CC -----
CC EMBL: D90908; BAAL7668.1; -.
CC PIR: S77110; S77110.

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DR InterPro: IPR007113; Cupin_sup.
DR InterPro: IPR003829; DUF209.
DR Pfam: PF03678; Pirin; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 232 AA; 25700 MW; 09B9DCC65352A470 CRC64;
Query Match 70.4%; Score 38; DB 1; Length 232;
Best Local Similarity 60.0%; Pred. No. 3.2;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 EYLVPPQGGF 10
DB 45 EDYIAPGGGF 54
RESULT 11
ERB4_MOUSE
ID ERB4_MOUSE STANDARD; PRT; 95 AA.
AC Q61527;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Receptor protein-tyrosine kinase erbB-4 (EC 2.7.1.112) (Fragments).
GN ERB4 OR MER4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-27 FROM N.A. (ISOFORMS JM-A AND JM-B).
RC TISSUE=Heart, and Kidney;
RX MEDLINE=97476287; PubMed=9334263;
RA Elenius K., Corfas G., Paul S., Choi C.J., Rio C., Plowman G.D.,
RA Klagsbrun M.;
RT "A novel juxtamembrane domain isoform of HER4/ErbB4. Isoform-specific
RT tissue distribution and differential processing in response to
RT phorbol ester.";
RL J. Biol. Chem. 272:26761-26768(1997).
RN [2]
RP SEQUENCE OF 28-95 FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=96069911; PubMed=7589796;
RA Moscote L.M., Chu G.C., Gautam M., Noakes P.G., Merlie J.P.,
RA Sanes J.R.;
RT "Synapse-associated expression of an acetylcholine receptor-inducing
RT protein, ARIA/herregulin, and its putative receptors, ErbB2 and ErbB3,
RT in developing mammalian muscle.";
RL Dev. Biol. 172:158-169(1995).
CC -!- FUNCTION: Specifically binds and is activated by neuregulins, NRG-
CC 2, NRG-3, heparin-binding EGF-LIKE growth factor, betacellulin and
CC NTAK. Interaction with these factors induces cell differentiation.
CC Not activated by EGF, TGF-A, and amphiregulin (by similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBUNIT: Homodimer or heterodimer with each of the other ERBB
CC receptors. Interacts with the PDZ domain of the syntrophin SNTB2
CC (by similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Comment=The 2 isoforms differ functionally in their response to
CC phorbol ester: isoform JM-A is processed but not isoform JM-B.
CC So, they respectively represent cleavable and noncleavable
CC forms of the receptor. Both isoforms are expressed in
CC cerebellum, cerebral cortex, spinal cord, medulla oblongata,
CC and eye, but the kidney expresses solely isoform JM-A and the
CC heart solely isoform JM-B;
CC Name=JM-A;
CC IsoID=Q61527-1; Sequence=Displayed;
CC Name=JM-B;
CC IsoID=Q61527-2; Sequence=VSP_002896;
CC -!- PTM: Ligand-binding increases phosphorylation on tyrosine
CC residues.

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CC -I- INDUCTION: By retinoic acid.
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CC -I- SIMILARITY: BELONGS TO THE TRANSGLUTAMINASE FAMILY.
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CC -----
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CC -----
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DR EMBL; X60686; CAA43097.1; ..
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DR PIR; S19680; SI9680.
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DR HSP; P00488; IQRK.
```

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DR InterPro; IPR001102; GluttransfG.
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DR InterPro; IPR002931; TrnsglumasE_like.
```

```
DR Pfam; PF01841; Transglut_core_1.
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```
DR Pfam; PF00927; Transglutamin_C; 2.
```

```
DR Pfam; PF00868; Transglutamin_N; 1.
```

```
DR SMART; SM00460; TGC; 1.
```

```
DR PROSITE; PS00547; TRANSLGLUTAMINASES; 1.
```

```
KW Transferase; Acyltransferase; Calcium-binding.
```

```
FT ACT_SITE 277 277 BY SIMILARITY.
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FT ACT_SITE 335 335 BY SIMILARITY.
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FT ACT_SITE 358 358 BY SIMILARITY.
```

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FT METAL 398 398 CALCIUM (BY SIMILARITY).
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FT METAL 400 400 CALCIUM (BY SIMILARITY).
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FT METAL 447 447 CALCIUM (BY SIMILARITY).
```

```
FT METAL 452 452 CALCIUM (BY SIMILARITY).
```

```
SQ SEQUENCE      587 AA; 77112 MW; 7BBA00F15E77994A CRC64;
```

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Query Match          68.5%; Score 37; DB 1; Length 687;  
Best Local Similarity 60.0%; Pred. No. 15;  
Matches    6; Conservative     3; Mismatches   1; Indels   0; Gaps   0;
```

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QY       1 EEYLVPQQGF 10  
DB      157 QEYVLTPQQGF 166  
         :|::|||  

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```
RESULT 13  
TMGM2_HUMAN
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```
ID TMGM2_HUMAN STANDARD; PRT; 687 AA.  
AC F21980; Q16436; O9BTN7; Q9UH35;  
DT 01-AUG-1991 (Rel. 19, Created)  
DI 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) (Tissue transglutaminase) (TGase C) (TGC) (TG(C)) (Transglutaminase 2) (TGase-H).  
GN TGm2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
NCBI_TaxID=9606;  
[1]  
SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.  
TISSUE=Endothelial cells;  
RX MEDLINE=91093168; PubMed=1670766;  
RA Gentile V., Saydak M., Chiocci A.A., Akande O., Birckbihler P.J., Lee K.N., Stein J.P., Davies P.J.A.; "Isolation and characterization of cDNA clones to mouse macrophage and human endothelial cell tissue transglutinases.";  
J. Biol. Chem. 266:478-483(1991). [2]  
SEQUENCE FROM N.A. (ISOFORM 2).  
RX MEDLINE=93054562; PubMed=135880;  
RA Fraij B.M., Birckbihler P.J., Patterson M.K. Jr., Lee K.N., Gonzales R.A.; "A retinoic acid-inducible mRNA from human erythro leukemia cells encodes a novel tissue transglutaminase homologue.";  
J. Biol. Chem. 267:22616-22623(1992). [3]
```


SEQUENCE FROM N.A. (ISOFORM 3).
 MEDLINE=96201707; PubMed=8611626;
 "A third human tissue transglutaminase homologue as a result of
 alternative gene transcripts.";
 RL Biochim. Biophys. Acta 1306:63-74(1996).
 [4]
 SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
 MEDLINE=21638749; PubMed=11780052;
 RA Jones M., Stavrides G., Almeida J.P., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Deloukas P., Matthews L.H., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C.N., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leivaeslath M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConnachie L.J., McLeay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
 RA Skuwn C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RA "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 [5]
 SEQUENCE FROM N.A. (ISOFORM 2).
 TISSUE=Kidney;
 RX MEDLINE=2238257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
 RA Fanev J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smallos D.E.,
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: CATALYZES THE CROSS-LINKING OF PROTEINS AND THE
 CC CONJUGATION OF POLYAMINES TO PROTEINS.
 CC -!- CATALYTIC ACTIVITY: Protein glutamine + alkylamine = protein N(5)-
 CC alkylglutamine + NH(3).
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -!- SUBUNIT: Monomer.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms-3;
 CC Name=1;
 CC IsoId=P21980-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P21980-2; Sequence=VSP_006411, VSP_006412;
 CC Name=3; Synonyms=TGH2;

CC IsoId=P21980-3; Sequence=VSP_006413, VSP_006414;
 CC -!- INDUCTION: By retinoic acid.
 CC -!- SIMILARITY: BELONGS TO THE TRANSGLUTAMINASE FAMILY.
 CC
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 CC
 CC EMBL; M55153; AAA63261.1; -
 DR EMBL; M98478; AAA36739.1; -
 DR EMBL; S81734; AAB36379.1; -
 DR EMBL; AL031651; CAB66115.1; -
 DR EMBL; AL031651; CAB66116.1; -
 DR EMBL; BC003551; AAH03551.1; -
 DR EMBL; A39045; A39045.
 DR PIR; S68092; S68092.
 DR PDB; 1FAU; 21-JUL-00.
 DR PDB; 1KV3; 13-MAR-02.
 DR Genew; HGNC:11778; TGM2.
 DR MIM; 190196; -
 DR GO; GO:0006464; P:protein modification; TAS.
 DR InterPro; IPR001102; Gluttransfg.
 DR InterPro; IPR002931; Trnsglutamase_like.
 DR Pfam; PF01841; Transglut_core; 1
 DR Pfam; PF00927; Transglutamin_C; 2.
 DR Pfam; PF00868; Transglutamin_N; 1.
 DR SMART; SM00460; TGC; 1.
 DR PROSITE; PS00547; TRANSGLUTAMINASES; 1.
 KW Transferase; Acyltransferase; Calcium-binding; Alternative splicing;
 KW 3D-structure.
 FT ACT_SITE 277 277 BY SIMILARITY.
 FT ACT_SITE 335 335 BY SIMILARITY.
 FT ACT_SITE 358 358 BY SIMILARITY.
 FT METAL 398 398 CALCIUM (BY SIMILARITY).
 FT METAL 400 400 CALCIUM (BY SIMILARITY).
 FT METAL 447 447 CALCIUM (BY SIMILARITY).
 FT METAL 452 452 CALCIUM (BY SIMILARITY).
 FT VARSPPLIC 539 548 EKVPLCILEY -> GKALCSWSIC (in isoform 2).
 FT VARSPPLIC 549 687 Missing (in isoform 2).
 FT VARSPPLIC 687 Missing (in isoform 3).
 FT VARSPPLIC 687 Missing (in isoform 3).
 FT VARSPPLIC 687 Missing (in isoform 3).
 FT CONFLICT 51 E -> Q (IN REF. 1).
 FT CONFLICT 186 E -> Q (IN REF. 1).
 FT CONFLICT 224 V -> G (IN REF. 1).
 FT CONFLICT 533 N -> T (IN REF. 1).
 FT CONFLICT 655 L -> V (IN REF. 1).
 SQ SEQUENCE 687 AA; 77328 MW; 7DA33FF35DE7B37 CRC64;
 Query Match 68.5%; Score 37; DB 1; Length 687;
 Best Local Similarity 60.0%; Pred. No. 15;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 BEYLVPQOGF 10
 Db 157 QEYVLTQOGF 166
 RESULT 14
 TGM2_CAVCU
 ID TGM2_CAVCU STANDARD; PRT; 689 AA.
 AC P08587;
 DT 01-AUG-1988 (Rel. 08, Created)

lung, salivary gland, and pancreas.
 -1- PTM: Ligand-binding increases phosphorylation on tyrosine residues.
 -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.

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 EMBL: L07868; AAB59446.1; .
 PIR: A47253; A47253.
 HSSP: P11362; 1FGK.
 Genew: HGNC:3432; ERBB4.
 MIM: 600543; .
 GO: GO:0005887; C: Integral to plasma membrane; TAS.
 GO: GO:0008283; P: cell proliferation; TAS.
 GO: GO:0007275; P: development; TAS.
 GO: GO:0007048; P: oncogenesis; TAS.
 InterPro: IPR000494; EGFR_L_domain.
 InterPro: IPR008211; Furin-like.
 InterPro: IPR006212; Furin-repeat.
 InterPro: IPR000719; Prot_kinase.
 InterPro: IPR001245; Tyr_kinase.
 InterPro: IPR004019; VLP_motif.
 Pfam: PF00757; Furin-like; 1.
 Pfam: PF00069; kinase; 1.
 Pfam: PF01030; Recep_L_domain; 2.
 Pfam: PF02757; VLP; 2.
 PRINTS: PD00109; TYRKINASE.
 ProDom: PD000001; Prot_kinase; 1.
 SMART: SM00261; FU; 5.
 SMART: SM00219; TykC; 1.
 PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 Transmembrane: Glycoprotein; Multigene family; Receptor; Signal;
 KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Alternative splicing.
 FT SIGNAL 1 25
 FT CHAIN 26 1308
 FT DOMAIN 26 651
 FT TRANSMEM 652 675
 FT DOMAIN 676 1308
 FT DOMAIN 186 334
 FT DOMAIN 496 633
 FT DOMAIN 718 985
 FT NP_BIND 724 732
 FT BINDING 751 751
 FT ACT_SITE 843 843
 FT DISULFID 189 197
 FT DISULFID 193 205
 FT DISULFID 213 221
 FT DISULFID 217 229
 FT DISULFID 230 238
 FT DISULFID 234 246
 FT DISULFID 249 258
 FT DISULFID 262 289
 FT DISULFID 293 304
 FT DISULFID 308 323
 FT DISULFID 326 330
 FT DISULFID 503 512
 FT DISULFID 507 520
 FT DISULFID 523 532
 FT DISULFID 536 552
 FT DISULFID 555 569
 FT DISULFID 559 577
 FT DISULFID 580 589
 FT DISULFID 593 614
 FT DISULFID 617 625

FT DISULFID 621 633 BY SIMILARITY.
 FT MOD_RES 1162 1182 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 1188 1188 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 1258 1258 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 1284 1284 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 253 253 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 358 358 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 410 410 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 473 473 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 495 495 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 548 548 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 576 576 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARSPLIC 626 648 NGPTSHDCIYPWTGCHSTLPQHA -> IGSIEDICIGLMD
 (in isoform JM-B).
 FT FT /FTid=VSP_002895.
 SQ SEQUENCE 1308 AA; 146807 MW; 5E4AE80985D88761 CRC64;

Query Match 68.5%; Score 37; DB 1; Length 1308;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEVLVPQ 7
 |||||
 Db 1020 EEVLVPQ 1026

Search completed: July 28, 2003, 17:04:13
 Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2003, 17:00:40 ; Search time 40 Seconds
(without alignments)
24.042 Million cell updates/sec

Title: US-09-930-125-3
Perfect score: 54
Sequence: 1 EYLVPPQGGF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	54	100.0	1254	2 I48161	p-185 precursor -
2	54	100.0	1255	1 A24571	protein-tyrosine k
3	54	100.0	1260	1 TVRTNU	protein-tyrosine k
4	50	92.6	1210	1 GQHUE	epidermal growth f
5	50	92.6	1210	2 A53183	epidermal growth f
6	46	85.2	540	1 TVFVEB	protein-tyrosine k
7	46	85.2	540	2 B44776	protein-tyrosine k
8	46	85.2	544	2 S35745	kinase-related tra
9	46	85.2	545	2 S00727	protein-tyrosine k
10	46	85.2	604	1 TVYUJH	protein-tyrosine k
11	46	85.2	698	1 TVFVLV	protein-tyrosine k
12	46	85.2	1223	1 TVCHLV	epidermal growth f
13	38	70.4	232	2 S77110	hypothetical prote
14	37	68.5	349	2 S68092	protein-glutamine
15	37	68.5	428	2 AE1611	probable proteinase
16	37	68.5	428	2 A11248	probable proteinase
17	37	68.5	548	2 A43502	protein-glutamine
18	37	68.5	687	1 A39045	protein-glutamine
19	37	68.5	687	1 S19680	protein-glutamine
20	37	68.5	691	1 A29996	protein-glutamine
21	37	68.5	751	2 T20733	hypothetical prote
22	37	68.5	1308	2 A47253	epidermal growth f
23	36	66.7	436	2 E90261	hypothetical prote
24	35	64.8	123	2 T50142	probable phosphogl
25	35	64.8	209	2 T37764	probable phosphogl
26	35	64.8	391	2 B48085	CAU1 protein - yea
27	35	64.8	687	1 B39045	protein-glutamine
28	35	64.8	917	1 R0MUNH	nitrate reductase
29	35	64.8	1242	2 S51246	probable DNA repai

30 34 63.0 262 2 B71817
31 34 63.0 330 2 D75032
32 34 63.0 431 2 AG2105
33 34 63.0 432 2 D95369
34 34 63.0 518 2 B86372
35 34 63.0 541 2 A48717
36 34 63.0 598 2 S55014
37 34 63.0 768 2 JC7352
38 34 63.0 988 1 TOEC21
39 34 63.0 997 2 S73556
40 34 63.0 1019 2 JC7538
41 34 63.0 1097 2 A29943
42 34 63.0 2290 1 GNNYE
43 34 63.0 2292 1 GNNYED
44 34 63.0 2292 1 GNNYED
45 34 63.0 2292 2 S35961

ALIGNMENTS

RESULT 1
I48161

p-185 precursor - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C:Accession: I48161

R:Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Y.; Ishik.
Gene 140, 251-255, 1994

A:Title: Cloning and activation of the Syrian hamster neu proto-oncogene.
A:Reference number: I48161; MUID:94193007; PMID:7908275

A:Accession: I48161

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-1254 <RES>

A:Cross-references: GB:D16295; NID:9493236; PIDN:BAA03801.1; PID:g747595

C:Genetics:

C:Superfamily: epidermal growth factor receptor; protein kinase homology

C:Keywords: ATP

F:718-983/Domain: protein kinase homology <KIN>

F:726-734/Region: protein kinase ATP-binding motif

Query Match

Best Local Similarity 100.0%; Score 54; DB 2; Length 1254;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPPQGGF 10

Db 1021 EYLVPPQGGF 1030

RESULT 2

A24571

protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human

N:Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein e

C:Species: Homo sapiens (man)

C:Date: 25-Oct-1987 #sequence_revision 06-Dec-1996 #text_change 11-Jun-1999

C:Accession: A24571; A25491; A44188; B41188; I59509; I57622

R:Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T

Nature 319, 230-234, 1986

A:Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth

A:Reference number: A24571; MUID:86118663; PMID:3003577

A:Accession: A24571

A:Molecule type: mRNA

A:Residues: 1-1255 <YAM>

A:Cross-references: GB:X03363; NID:q31197; PIDN:CAA27060.1; PID:g31198

R:Semba, K.; Kanata, N.; Toyoshima, K.; Yamamoto, T.

Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985

A:Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epid

A:Reference number: A25491; MUID:86016729; PMID:2995967

A:Accession: A25491

hypothetical prote
anion transporting
4-aminobutyrate am
conserved hypothet
protein F508.34 11
glutamate formimid
NADH2 dehydrogenas
glucose-regulated
transposase - Esch
MG414 homolog C12-
neuronal different
Toll protein precu
genome polyprotein
genome polyprotein
genome polyprotein
capsid polyprotein

A:Residues: 737-1031 <SEM>
A:Cross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:g553282
R:Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg, P.
Science 230, 1132-1139, 1985
A:Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chromosomal location with erbB-2
A:Reference number: A44188; MUID:86070181; PMID:2999974
A:Accession: A44188
A:Molecule type: DNA
A:Residues: 740-910 <COU1>
A:Cross-references: GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:g183989
A:Accession: B44188
A:Molecule type: mRNA
A:Residues: 1-517, 'RALL', 522, 'S', 524-654, 'V', 656-1169, 'A', 1171-1255 <COU2>
A:Cross-references: GB:M11730; NID:g183986
R:King, C.R.; Kraus, M.H.; Aaronson, S.A.
Science 229, 974-976, 1985
A:Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma.
A:Reference number: 159509; MUID:85272597; PMID:2992089
A:Accession: 159509
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 832-909 <REX>
A:Cross-references: GB:L29395; NID:g459807; PIDN:AAA35809.1; PID:g459808
R:Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
Mol. Cell. Biol. 7, 2597-2601, 1987
A:Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptional regulation
A:Reference number: 157622; MUID:87286898; PMID:3039351
A:Accession: 157622
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-191 <TAL>
A:Cross-references: GB:M16792; NID:g183983; PIDN:AAA58637.1; PID:g553332
A:Comment: Amplification and overexpression of this erbB-related gene occurs in about 30% of human breast carcinomas
C:Genetics:
A:Gene: GDB:ERBB2; NGL: NEU; HER-2
A:Map position: 17q21.1-17q21.1
A:Introns: 25/1; 75/3; 147/1; 883/3
A:Note: the list of introns is incomplete
C:Function:
A:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C:Superfamily: epidermal growth factor receptor; protein kinase homology
C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphotyrosine
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <MAT>
F:22-653/Domain: extracellular #status predicted <EXT>
F:770-304/Domain: EGF receptor extracellular domain repeat <EE1>
F:395-605/Domain: EGF receptor extracellular domain repeat <EE2>
F:654-675/Domain: transmembrane #status predicted <TM>
F:676-1255/Domain: intracellular #status predicted <INT>
F:718-983/Domain: protein kinase homology <KIN>
F:726-734/Region: protein kinase ATP-binding motif
F:681,124,187,259,530,571,629/Binding site: carboxylate (Asn) (covalent) #status predicted
F:686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:753/Active site: Lys #status predicted
F:1139,1221,1222,1248/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)

Query Match 100.08; Score 54; DB 1; Length 1255;
Best Local Similarity 100.08; Pred. No. 0.033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLPQOGF 10
|||||
DB 1021 EBYLPQOGF 1030

RESULT 3

TVRTNU

protein-tyrosine kinase (EC 2.7.1.112) neu precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 11-Jun-1999

C:Accession: A24562; A61204

R:Bargmann, C.I.; Hung, M.C.; Weinberg, R.A.
Nature 319, 226-230, 1986
A:Title: The neu oncogene encodes an epidermal growth factor receptor-related protein
A:Reference number: A24562; MUID:86118662; PMID:3945311
A:Accession: A24562
A:Molecule type: mRNA
A:Residues: 1-1260 <BAR>
A:Cross-references: EMBL:X03362; NID:g56745; PIDN:CAA27059.1; PID:g56746
R:Masui, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Col
Carcinogenesis 12, 1975-1978, 1991
A:Title: Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals a thiazolylformamide or N-methyl-N-nitrosourea
A:Reference number: A61204; MUID:92035293; PMID:1682063
A:Accession: A61204
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 637-663, 'V', 665-702 <MAS>
A:Note: authors translated the codon GCA for residue 25 as Val
C:Genetics:
A:Gene: neu
C:Superfamily: epidermal growth factor receptor; protein kinase homology
C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphotyrosine
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1260/Product: protein-tyrosine kinase neu #status predicted <MAT>
F:658-680/Domain: transmembrane #status predicted <TM>
F:723-988/Domain: protein kinase homology <KIN>
F:731-739/Region: protein kinase ATP-binding motif
F:71,191,263,535,576,634/Binding site: carboxylate (Asn) (covalent) #status predicted
F:691/Binding site: phosphate (Thr) (covalent) #status predicted
F:758/Active site: Lys #status predicted
F:782,1227,1253/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 100.08; Score 54; DB 1; Length 1260;
Best Local Similarity 100.08; Pred. No. 0.033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLPQOGF 10
|||||
DB 1026 EBYLPQOGF 1035

RESULT 4

GDHUE

epidermal growth factor receptor precursor - human

N:Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB

C:Species: Homo sapiens (man)

C>Date: 15-Nov-1984 #sequence_revision 27-Nov-1985 #text_change 11-Jun-1999

C:Accession: A00641; A25772; S30024; A38672; A00642; A43615; A23062; A05281; A60143

R:Ullrich, A.; Coussens, L.; Hayflick, J.S.; Dull, T.J.; Gray, A.; Tam, A.W.; Lee, R.P.H.

Nature 309, 418-425, 1984

A:Title: Human epidermal growth factor receptor cDNA sequence and aberrant expression

A:Reference number: A00641; MUID:84219729; PMID:6328312

A:Accession: A00641

A:Molecule type: mRNA

A:Residues: 1-1210 <ULL>

A:Cross-references: EMBL:X00588; NID:g31113; PIDN:CAA25240.1; PID:g757924

A:Note: the authors translated the codon AAG for residue 540 as Asn

R:Ishii, S.; Xu, Y.; Stratton, R.H.; Roe, B.A.; Merlino, G.T.; Pastan, I.

Proc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985

A:Title: Characterization and sequence of the promoter region of the human epiderma

A:Reference number: A25772; MUID:85270438; PMID:2991899

A:Accession: A25772

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-29 <ISH>

A:Cross-references: GB:M11234; NID:g181981; PIDN:AAA52370.1; PID:g553272

R:Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Waterfield, M.

Oncogene Res. 1, 375-396, 1987

A:Title: The human EGF receptor gene: structure of the 110 kb locus and identification

A:Reference number: S30024; MUID:88217333; PMID:3329716

A:Accession: S30024

A:Molecule type: DNA

A:Residues: 1-29 <HA2>
A:Cross-references: EMBL:X06370; NID:g31118; PIDN:CAA29668.1; PID:g31119
R:Haley, J.D.; Waterfield, M.D.
J. Biol. Chem. 266, 1746-1753, 1991
A:Title: Contributory effects of de Novo transcription and premature transcript termination
A:Reference number: A38672; MUID:91107677; PMID:1988448
A:Accession: A38672
A:Molecule type: DNA
A:Residues: 1-29 <HAL>
A:Cross-references: GB:M38425; NID:g181977; PIDN:AAA63171.1; PID:g553271
A:Experimental source: carcinoma cell line A431-7
R:Xu, Y.; Ishii, S.; Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Roe, B.A.; Merl Nature 309, 806-810, 1984
A:Title: Human epidermal growth factor receptor cDNA is homologous to a variety of RNAs
A:Reference number: A00642; MUID:84245835; PMID:6330563
A:Accession: A00642
A:Molecule type: mRNA
A:Residues: 'RCNWRRA', 150-187, 'KSVIQAV', 195, 'M', 197, 'A', 199-222, 'S', 224-304, 'RA', 307-321, '798-799, 'TD', 802-811, 'R', 813-942 <XUY>
A:Experimental source: A431 human carcinoma cells, which have large numbers of EGF receptor
R:Lin, C.R.; Chen, W.S.; Krueger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, I. Science 224, 843-848, 1984
A:Title: Expression cloning of human EGF receptor complementary DNA: gene amplification
A:Reference number: A43615; MUID:84196372; PMID:6326261
A:Accession: A43615
A:Molecule type: mRNA
A:Residues: 713-964 <LIN>
A:Experimental source: epidermoid carcinoma cell line A431
R:Simmen, F.A.; Gope, M.L.; Schulz, T.Z.; Wright, D.A.; Carpenter, G.; O'Malley, B.W. Biochem. Biophys. Res. Commun. 124, 125-132, 1984
A:Reference number: A23062; MUID:85046483; PMID:6093780
A:Accession: A23062
A:Molecule type: mRNA
A:Residues: 1028-1210 <STM>
R:Weber, W.; Gill, G.N.; Speiss, J. Science 224, 294-297, 1984
A:Reference number: A05281; MUID:84172183; PMID:6324343
A:Accession: A05281
A:Molecule type: protein
A:Residues: 25-30, 'S', 32-51, 454-467 <WEB>
R:Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros, J.V. J. Biol. Chem. 260, 5205-5208, 1985
A:Title: Identification of residues in the nucleotide binding site of the epidermal growth factor receptor
A:Reference number: A60143; MUID:85182650; PMID:2985580
A:Accession: A60143
A:Molecule type: protein
A:Residues: 740-744, 'X', 746-747 <RUS>
R:Mroczkowski, B.; Mosig, G.; Cohen, S. Nature 309, 270-273, 1984
A:Title: ATP-stimulated interaction between epidermal growth factor receptor and superoxide dismutase
A:Reference number: A38023; MUID:84191554; PMID:6325948
A:Contents: annotation; receptor activity
A:Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DNA
R:Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; Der, C.J. Cell 59, 33-43, 1989
A:Title: Functional independence of the epidermal growth factor receptor from a domain in the EGF receptor
A:Reference number: A33331; MUID:90003233; PMID:2790960
A:Contents: annotation; internalization signal
C:Comment: Binding of EGF to the receptor leads to internalization of the EGF-receptor complex
C:Genetics:
A:Gene: GDB:EGFR
A:Cross-references: GDB:120610; OMIM:131550
A:Map position: 7p12.3-7p12.1
C:Superfamily: epidermal growth factor receptor; protein kinase homology
C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphotyrosine
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-1210/Product: EGF receptor #status predicted <NAT>
F:25-645/Domain: extracellular #status predicted <EXT>
F:75-300/Domain: EGF receptor extracellular domain repeat <EE1>
F:390-600/Domain: EGF receptor extracellular domain repeat <EE2>
F:646-668/Domain: transmembrane #status predicted <TM>
F:669-1210/Domain: intracellular #status predicted <INT>
F:710-975/Domain: protein kinase homology <KIN>

F:718-726/Region: protein kinase ATP-binding motif
F:999-1046/Region: coated-pit mediated internalization signal
F:1047-1210/Region: inhibitory
F:128, 175, 352, 413, 444, 528, 603/Binding site: carbohydrate (Asn) (covalent) #status p
F:745/Active site: Lys #status experimental
Query Match 92.6%; Score 50; DB 1; Length 1210;
Best Local Similarity 80.0%; Pred. No. 0.19;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 EBYLPQOGF 10
DB 1014 DEYLPQOGF 1023
RESULT 5
A53183
epidermal growth factor receptor precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 18-Jun-1999
C:Accession: A53183; A43818; S24942; A28941; S45325; I49643
R:Luetke, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jenkins, N Genes Dev. 8, 399-413, 1994
A:Title: The mouse waved-2 phenotype results from a point mutation in the EGF receptor
A:Reference number: A53183; MUID:94170986; PMID:8125255
A:Accession: A53183
A:Molecule type: mRNA
A:Residues: 1-1210 <LUE>
A:Cross-references: GB:U03425
R:Avivi, A.; Lax, I.; Ullrich, A.; Schlessinger, J.; Givol, D.; Morse, B. Oncogene 6, 673-676, 1991
A:Title: Comparison of EGF receptor sequences as a guide to study the ligand binding site
A:Reference number: A43818; MUID:91232866; PMID:2030916
A:Accession: A43818
A:Molecule type: mRNA
A:Residues: 1-714 <AVI>
A:Cross-references: GB:X59698
R:Eisinger, D.P.; Serrero, G. submitted to the EMBL Data Library, June 1992
A:Reference number: S24942
A:Accession: S24942
A:Molecule type: mRNA
A:Residues: 969-971, 'K', 973-1115, 'D' <EIS>
A:Cross-references: EMBL:Z12608
R:Heisermann, G.J.; Gill, G.N. J. Biol. Chem. 263, 13152-13158, 1988
A:Title: Epidermal growth factor receptor threonine and serine residues phosphorylated by protein kinase C
A:Reference number: A28941; MUID:88330814; PMID:3138233
A:Accession: A28941
A:Molecule type: protein
A:Residues: 689-694, 'X', 696-704, 'L', 706-707; 989-992, 'XX', 995-996, 'X', 998-1000; 1002-1004, 'X', 1006-1007, 'X', 1009-1010, 'X', 1012-1013, 'X', 1015-1016, 'X', 1018-1019, 'X', 1021-1022, 'X', 1024-1025, 'X', 1027-1028, 'X', 1030-1031, 'X', 1033-1034, 'X', 1036-1037, 'X', 1039-1040, 'X', 1042-1043, 'X', 1045-1046, 'X', 1048-1049, 'X', 1051-1052, 'X', 1054-1055, 'X', 1057-1058, 'X', 1060-1061, 'X', 1063-1064, 'X', 1066-1067, 'X', 1069-1070, 'X', 1072-1073, 'X', 1075-1076, 'X', 1078-1079, 'X', 1081-1082, 'X', 1084-1085, 'X', 1087-1088, 'X', 1090-1091, 'X', 1093-1094, 'X', 1096-1097, 'X', 1099-1100, 'X', 1102-1103, 'X', 1105-1106, 'X', 1108-1109, 'X', 1111-1112, 'X', 1114-1115, 'X', 1117-1118, 'X', 1120-1121, 'X', 1123-1124, 'X', 1126-1127, 'X', 1129-1130, 'X', 1132-1133, 'X', 1135-1136, 'X', 1138-1139, 'X', 1141-1142, 'X', 1144-1145, 'X', 1147-1148, 'X', 1150-1151, 'X', 1153-1154, 'X', 1156-1157, 'X', 1159-1160, 'X', 1162-1163, 'X', 1165-1166, 'X', 1168-1169, 'X', 1171-1172, 'X', 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F:1-24/Domain: signal sequence #status predicted <SIG>
 F:648-670/Domain: transmembrane #status predicted <TM>
 F:713-977/Domain: protein kinase homology <KIN>
 F:720-728/Region: protein kinase ATP-binding motif
 F:680-695/Binding site: phosphate (Thr) (covalent) #status experimental
 F:697,1070,1071/Binding site: phosphate (Ser) (covalent) #status experimental
 F:993/Binding site: (or 997) phosphate (Ser) (covalent) #status experimental
 F:1028/Binding site: (or 1030 or 1032) phosphate (Ser) (covalent) #status experimental
 F:1197/Binding site: phosphate (Tyr) (covalent) #status experimental

Query Match 92.6%; Score 50; DB 2; Length 1210;
 Best Local Similarity 80.0%; Pred. No. 0.19;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEYLVPOQGF 10
 :|||||
 Db 1016 DEYLVPHQGF 1025

RESULT 6

TVFVB

protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus (strain ES4)
 C:Species: avian erythroblastosis virus
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jun-1999

C:Accession: A25231; B25231
 R:Choi, O.R.; Trainor, C.; Graf, T.; Beug, H.; Engel, J.D.

Mol. Cell. Biol. 6, 1751-1759, 1986

A:Title: A single amino acid substitution in v-erbB confers a thermolabile phenotype to

A:Reference number: A25231; MUID:87064458; PMID:2878364

A:Accession: A25231

A:Molecule type: DNA

A:Residues: 1-540 <CHO>

A:Cross-references: GB:M13179; NID:q209679; PIDN:AAA42401.1; PID:q209680

A:Note: the authors translated the codon AAG for residue 157 as Gly, ATG for residue 253

C:Genetics:

A:Gene: erbB

C:Superfamily: epidermal growth factor receptor; protein kinase homology

F:130-395/Domain: protein kinase homology

F:138-146/Region: protein kinase ATP-binding motif

F:165/Active site: Lys #status predicted

Query Match

Best Local Similarity 85.2%; Score 46; DB 1; Length 540;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEYLVPOQGF 10

:|||||

Db 434 DEYLVPHQGF 443

RESULT 7

B44776

protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus (strain ES4)
 C:Species: avian erythroblastosis virus
 C:Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 04-Feb-2000

C:Accession: B44776
 R:Bruskin, A.; Jackson, J.; Bishop, J.M.; McCarley, D.J.; Schatzman, R.C.

Oncogene 5, 15-24, 1990

A:Title: Six amino acids from the retroviral gene gag greatly enhance the transforming p

A:Reference number: A44776; MUID:90206603; PMID:1969616

A:Accession: B44776

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-540 <BRD>

A:Cross-references: GB:X52211

C:Genetics:

A:Gene: erbB

C:Superfamily: epidermal growth factor receptor; protein kinase homology

F:130-395/Domain: protein kinase homology

F:138-146/Region: protein kinase ATP-binding motif

F:165/Active site: Lys #status predicted

Query Match

Best Local Similarity 80.0%; Score 46; DB 2; Length 545;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEYLVPOQGF 10

:|||||

Db 439 DEYLVPHQGF 448

RESULT 10

TVFVB

protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus (strain H)
 C:Species: avian erythroblastosis virus

Query Match 85.2%; Score 46; DB 2; Length 540;
 Best Local Similarity 80.0%; Pred. No. 0.48;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEYLVPOQGF 10

:|||||

Db 434 DEYLVPHQGF 443

RESULT 8

S35745

protein-tyrosine kinase (EC 2.7.1.112) erbB - avian erythroblastosis virus
 C:Species: avian erythroblastosis virus
 C:Date: 03-Mar-1994 #sequence_revision 26-May-1995 #text_change 28-Feb-1997

C:Accession: S35745
 R:Vennstroem, B.

submitted to the EMBL Data Library, March 1993

A:Reference number: S35743

A:Accession: S35745

A:Molecule type: DNA

A:Residues: 1-544 <VEN>

A:Cross-references: EMBL:X12707

C:Genetics:

A:Gene: erbB

C:Superfamily: epidermal growth factor receptor; protein kinase homology
 C:Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specif

F:135-400/Domain: protein kinase homology <KIN>

F:143-151/Region: protein kinase ATP-binding motif

F:170/Active site: Lys #status predicted

F:170/Active site: Lys #status predicted

Query Match

Best Local Similarity 85.2%; Score 46; DB 2; Length 544;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEYLVPOQGF 10

:|||||

Db 439 DEYLVPHQGF 448

RESULT 9

S00727

kinase-related transforming protein (erbB) (EC 2.7.1.-) - avian erythroblastosis viru
 C:Species: avian erythroblastosis virus
 C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 28-Feb-1997

C:Accession: S00727
 R:Scotting, P.; Vennstrom, B.; Jansen, M.; Graf, T.; Beug, H.; Hayman, M.J.

Oncogene Res. 1, 265-278, 1987

A:Title: Common site of mutation in the erbB gene of avian erythroblastosis virus mut

A:Reference number: S00727; MUID:88217326; PMID:2897102

A:Accession: S00727

A:Molecule type: DNA

A:Residues: 1-545 <SCO>

A:Cross-references: EMBL:X06943

C:Genetics:

A:Gene: erbB

C:Superfamily: epidermal growth factor receptor; protein kinase homology

F:135-400/Domain: protein kinase homology <KIN>

F:143-151/Region: protein kinase ATP-binding motif

F:143-151/Region: protein kinase ATP-binding motif

Query Match

Best Local Similarity 85.2%; Score 46; DB 2; Length 545;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEYLVPOQGF 10

:|||||

Db 439 DEYLVPHQGF 448

C;Date: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 11-Jun-1999
 C;Accession: A00644; A38022
 R;Yamamoto, T.; Nishida, T.; Miyajima, N.; Kawai, S.; Ooi, T.; Toyoshima, K.
 Cell 35, 71-78, 1983
 A;Title: The erbB gene of avian erythroblastosis virus is a member of the src gene family
 A;Reference number: A00644; MUID:84026539; PMID:6313229
 A;Accession: A00644
 A;Molecule type: DNA
 A;Residues: 1-604 <YAM>
 A;Cross-references: GB:K01216; NID:g209676; PIDN:AAA2400.1; PID:g209678
 R;Debulre, B.; Henry, C.; Benalissa, M.; Biserte, G.; Claverie, J.M.; Saule, S.; Martin, Science 224, 1456-1459, 1984
 A;Title: Sequencing the erbA gene of avian erythroblastosis virus reveals a new type of
 A;Reference number: A38022; MUID:84232957; PMID:6328658
 A;Accession: A38022
 A;Molecule type: DNA
 A;Residues: 1-28, 'W', 30-139, 'F', 141-145, 'V', 147-152 <DEB>
 A;Cross-references: GB:K02006
 C;Genetics:
 A;Gene: erbB
 C;Superfamily: epidermal growth factor receptor; protein kinase homology
 C;Keywords: ATP; oncogene, phosphotransferase; transforming protein; tyrosine-specific P
 F:130-395/Domain: protein kinase homology <KIN>
 F:138-146/Region: protein kinase ATP-binding motif
 F:165/Active site: Lys #status predicted

Query Match 85.2%; Score 46; DB 1; Length 604;
 Best Local Similarity 80.0%; Pred. No. 0.55;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEYLPQGGF 10
 :|||||
 Db 434 DEYLPVHQGF 443
 :|||||
 RESULT 11
 TVFVLV
 N;Contains: amino end of gag protein; env protein fragment; protein-tyrosine kinase
 C;Species: avian leukosis virus, ALV
 C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jun-1999
 C;Accession: B00643; A00643
 R;Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raines, M
 Cell 41, 719-726, 1985
 A;Title: c-erbA activation in ALV-induced erythroblastosis: novel RNA processing and pro
 A;Reference number: A00643; MUID:85228222; PMID:2988784
 A;Accession: B00643
 A;Molecule type: mRNA
 A;Residues: 1-698 <NTIL>
 A;Cross-references: GB:M10066; GB:M13881; NID:g211749; PIDN:AAA48763.1; PID:g211750
 A;Note: in Genbank entry CHKERBFF, release 109.0, the source is designated as Gallus gal
 C;Comment: This protein is synthesized as a gag-env-erbB protein.
 C;Genetics:
 A;Gene: gag-env-erbB
 C;Superfamily: epidermal growth factor receptor; protein kinase homology
 C;Keywords: ATP; oncogene; phosphotransferase; transforming protein; tyrosine-specific P
 F:1-6/Product: gag protein (fragment) #status predicted <GAG>
 F:7-59/Product: env protein (fragment) #status predicted <ENV>
 F:60-698/Product: protein-tyrosine kinase erbB #status predicted <ERB>
 F:194-459/Domain: protein kinase homology <KIN>
 F:202-210/Region: protein kinase ATP-binding motif
 F:229/Active site: Lys #status predicted

Query Match 85.2%; Score 46; DB 1; Length 698;
 Best Local Similarity 80.0%; Pred. No. 0.64;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEYLPQGGF 10
 :|||||
 Db 498 DEYLPVHQGF 507
 :|||||
 RESULT 12

TVCHLV
 N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
 C;Species: Gallus gallus (chicken)
 C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000
 C;Accession: A27720; A00643
 R;Lax, I.; Johnson, A.; Howk, R.; Sap, J.; Bellot, F.; Winkler, M.; Ullrich, A.; Ven
 Mol. Cell. Biol. 8, 1970-1978, 1988
 A;Title: Chicken epidermal growth factor (EGF) receptor: cDNA cloning, expression in
 A;Reference number: A27720; MUID:86261272; PMID:3260329
 A;Accession: A27720
 A;Molecule type: mRNA
 A;Residues: 1-1223 <LAX>
 A;Cross-references: GB:M20386
 R;Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Rottman, F.M.; Crittenden, L.B.; Raine
 Cell 41, 719-726, 1985
 A;Title: c-erbB activation in ALV-induced erythroblastosis: novel RNA processing and
 A;Reference number: A00643; MUID:85228222; PMID:2988784
 A;Accession: A00643
 A;Molecule type: mRNA
 A;Residues: 585-1223 <NTIL>
 A;Cross-references: GB:M10066
 C;Genetics:
 A;Gene: erbB
 C;Superfamily: epidermal growth factor receptor; protein kinase homology
 C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth fac
 F:1-30/Domain: signal sequence #status predicted <SIG>
 F:31-1223/Product: epidermal growth factor receptor #status predicted <MAT>
 F:31-654/Domain: extracellular #status predicted <EXT>
 F:81-307/Domain: EGF receptor extracellular domain repeat <EEL>
 F:397-610/Domain: EGF receptor extracellular domain repeat <EE2>
 F:655-677/Domain: EGF receptor extracellular domain repeat <EE2>
 F:678-1223/Domain: transmembrane #status predicted <TMW>
 F:719-984/Domain: intracellular #status predicted <INT>
 F:727-735/Region: protein kinase homology <KIN>
 F:136,202,280,361,370,422,575,580,615,635/Binding site: carbohydrate (Thr) (covalent);
 F:192,650/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F:687/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
 F:754/Active site: Lys #status predicted
 F:1100,1183,1208/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #
 Query Match 85.2%; Score 46; DB 1; Length 1223;
 Best Local Similarity 80.0%; Pred. No. 1.2;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEYLPQGGF 10
 :|||||
 Db 1023 DEYLPVHQGF 1032
 :|||||
 RESULT 13
 S77110
 hypothetical protein sl11773 - Synechocystis sp. (strain PCC 6803)
 C;Species: Synechocystis sp.
 A;Variety: PCC 6803
 C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
 C;Accession: S77110
 R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
 O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
 DNA Res. 3, 109-136, 1996
 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
 S.
 A;Reference number: S74322; MUID:97061201; PMID:8905231
 A;Accession: S77110
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-232 <KAN>
 A;Cross-references: EMBL:D90908; GB:AB001339; NID:g1652725; PIDN:BAAL7668.1; PID:g165
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C;Superfamily: conserved hypothetical protein sl11773
 Query Match 70.4%; Score 38; DB 2; Length 232;

Best Local Similarity 60.0%; Pred. No. 7.1;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EYLVPOQGF 10
|:|:|
Db 45 EDYIAPQGF 54

RESULT 14

S68092

protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) 2, splice form 3 - human

C:Species: Homo sapiens (man)
C:Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text_change 05-May-2000
C:Accession: S68092
R:Frail, B.M.; Gonzales, R.A.
Biochim. Biophys. Acta 1306, 63-74, 1996
A:Title: A third human tissue transglutaminase homologue as a result of alternative gene
A:Reference number: S68092; MUID:96201707; PMID:8611626
A:Accession: S68092
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-349 <FRA>

A:Cross-references: GB:S81734; NID:g1478006; PIDN:AAB36379.1; PID:g1478007

C:Genetics:

A:Gene: GDB:TGM2

A:Cross-references: GDB:128013; OMIM:190196

A:Map position: 20q11.2-20q12

C:Keywords: alternative splicing; aminoacyltransferase

Query Match 68.5%; Score 37; DB 2; Length 349;
Best Local Similarity 60.0%; Pred. No. 18;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYLVPOQGF 10
|:|:|
Db 157 QEYVLTQGF 166

RESULT 15

AE1611

probable proteinase homolog lin1430 [imported] - Listeria innocua (strain Clip11262)

C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 17-May-2002
C:Accession: AE1611
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AE1077; MUID:21537279; PMID:11679669

A:Accession: AE1611

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-428 <GLA>

A:Cross-references: GB:AL592022; PIDN:CAC96661.1; PID:g16413903; GSPDB:GN00178

A:Experimental source: strain Clip11262

C:Genetics:

A:Gene: lin1430

C:Superfamily: mitochondrial processing peptidase alpha chain

Query Match 68.5%; Score 37; DB 2; Length 428;

Best Local Similarity 75.0%; Pred. No. 22;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLVPOQGF 10
|:|:|
Db 25 YLLPKQGF 32

Search completed: July 28, 2003, 17:06:43
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2003, 17:06:05 ; Search time 50 seconds
(without alignments)
23.752 Million cell updates/sec

Title: US-09-930-125-3
Perfect score: 54
Sequence: 1 EYLVPPQGF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	10	10	US-09-930-125-3
2	54	100.0	59	10	US-09-854-356-5
3	54	100.0	266	10	US-09-854-356-4
4	54	100.0	293	15	US-10-102-806-583
5	54	100.0	583	10	US-09-930-125-8
6	54	100.0	587	10	US-09-930-125-10
7	54	100.0	589	10	US-09-930-125-11
8	54	100.0	600	10	US-09-854-356-7
9	54	100.0	712	10	US-09-854-356-6
10	54	100.0	919	10	US-09-854-356-5
11	54	100.0	1253	15	US-10-146-473-72
12	54	100.0	1255	9	US-09-811-123-9
13	54	100.0	1255	9	US-09-811-115-3
14	54	100.0	1255	10	US-09-769-508-2
15	54	100.0	1255	10	US-09-854-356-1

16	54	100.0	1255	10	US-09-930-125-2	Sequence 2, Appli
17	54	100.0	1255	11	US-09-441-411-6	Sequence 6, Appli
18	54	100.0	1255	15	US-10-207-655-45	Sequence 45, Appl
19	54	100.0	1255	15	US-10-177-293-126	Sequence 126, App
20	54	100.0	1256	10	US-09-854-356-2	Sequence 2, Appli
21	54	100.0	1256	10	US-09-854-356-14	Sequence 14, Appl
22	54	100.0	1260	10	US-09-870-759-118	Sequence 118, Appl
23	50	92.6	1210	9	US-09-725-433-2	Sequence 2, Appli
24	43	79.6	73	10	US-09-796-692-1649	Sequence 1649, Ap
25	43	79.6	73	10	US-09-796-692-2500	Sequence 2500, Ap
26	43	79.6	73	15	US-10-040-862-1649	Sequence 1649, Ap
27	43	79.6	73	15	US-10-040-862-2500	Sequence 2500, Ap
28	43	79.6	115	9	US-09-925-302-708	Sequence 708, App
29	37	68.5	687	14	US-10-029-654-10	Sequence 10, Appl
30	37	68.5	705	11	US-09-158-722-4	Sequence 4, Appli
31	37	68.5	1308	10	US-09-940-101-2	Sequence 2, Appli
32	37	68.5	1308	15	US-10-207-655-47	Sequence 47, Appl
33	36	66.7	461	9	US-09-925-299-957	Sequence 957, App
34	36	66.7	461	11	US-09-925-299-957	Sequence 957, App
35	36	66.7	461	15	US-10-106-698-5254	Sequence 5254, Ap
36	36	66.7	497	15	US-10-156-761-8691	Sequence 8691, Ap
37	34	63.0	30	9	US-09-864-761-46868	Sequence 46868, A
38	34	63.0	262	9	US-09-815-242-11607	Sequence 11607, A
39	33	61.1	72	9	US-09-864-761-41671	Sequence 41671, A
40	33	61.1	148	9	US-09-864-761-37790	Sequence 37790, A
41	33	61.1	219	15	US-10-156-761-9655	Sequence 9655, Ap
42	33	61.1	523	10	US-09-910-174A-11	Sequence 11, Appl
43	33	61.1	523	10	US-09-955-866-10	Sequence 10, Appl
44	33	61.1	523	10	US-09-896-738-16	Sequence 16, Appl
45	33	61.1	527	10	US-09-910-174A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-09-930-125-3
; Sequence 3, Application US/09930125
; Publication No. US20020193329A1
; GENERAL INFORMATION:
; APPLICANT: Hand-Zimmerman, Susan
; APPLICANT: Cheever, Martin A.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Vedvick, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.544
; CURRENT APPLICATION NUMBER: US/09/930,125
; CURRENT FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-125-3

Query Match 100.0%; Score 54; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPPQGF 10
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Db 1 EYLVPPQGF 10
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RESULT 2

US-09-854-356-5
; Sequence 5, Application US/09854356
; Patent No. US2002017567A1

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; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Gheysen, Dirk
; APPLICANT: Corixa Corporation
; APPLICANT: Smithkline Beecham Biologicals S. A.
; TITLE OF INVENTION: HER-2/neu Fusion Proteins
; FILE REFERENCE: 014058-009810PC
; CURRENT APPLICATION NUMBER: US/09/854,356
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 09/493,480
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,976
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: fragment of the phosphorylation domain, preferred
; OTHER INFORMATION: portion (delta PD) of human HER-2/neu
US-09-854-356-5
Query Match 100.0%; Score 54; DB 10; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEYLVPOQGF 10
Db 32 EEYLVPOQGF 41
RESULT 3
US-09-854-356-4
; Sequence 4, Application US/09854356
; Patent No. US20020177567A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Gheysen, Dirk
; APPLICANT: Corixa Corporation
; APPLICANT: Smithkline Beecham Biologicals S. A.
; TITLE OF INVENTION: HER-2/neu Fusion Proteins
; FILE REFERENCE: 014058-009810PC
; CURRENT APPLICATION NUMBER: US/09/854,356
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 09/493,480
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,976
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: phosphorylation domain (PD) of human HER-2/neu
US-09-854-356-4
Query Match 100.0%; Score 54; DB 10; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEYLVPOQGF 10
Db 32 EEYLVPOQGF 41
RESULT 4
US-10-102-806-583
; Sequence 583, Application US/10102806
; Publication No. US20030054421A1
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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 583
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (52)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (53)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (58)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (150)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (171)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (207)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (254)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-583
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Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEYLVPOQGF 10
Db 105 EEYLVPOQGF 114
RESULT 5
US-09-930-125-9
; Sequence 9, Application US/09930125
; Publication No. US20020193329A1
; GENERAL INFORMATION:
; APPLICANT: Hand-Zimmerman, Susan
; APPLICANT: Cheever, Martin A.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Vedvick, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.544
; CURRENT APPLICATION NUMBER: US/09/930,125
; CURRENT FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 583
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-930-125-9

Query Match 100.0%; Score 54; DB 10; Length 583;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPOQGF 10
Db 347 EYLVPOQGF 356

RESULT 6

US-09-930-125-8
; Sequence 8, Application US/09930125
; Publication No. US20020193329A1

; GENERAL INFORMATION:

; APPLICANT: Hand-Zimmerman, Susan

; APPLICANT: Cheever, Martin A.

; APPLICANT: Foy, Teresa M.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Kalos, Michael D.

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Vedvick, Thomas S.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS

; FILE REFERENCE: 210121.544

; CURRENT APPLICATION NUMBER: US/09/930,125

; CURRENT FILING DATE: 2001-08-14

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 8

; LENGTH: 587

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-930-125-8

Query Match 100.0%; Score 54; DB 10; Length 587;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPOQGF 10
Db 347 EYLVPOQGF 356

RESULT 7

US-09-930-125-10
; Sequence 10, Application US/09930125
; Publication No. US20020193329A1

; GENERAL INFORMATION:

; APPLICANT: Hand-Zimmerman, Susan

; APPLICANT: Cheever, Martin A.

; APPLICANT: Foy, Teresa M.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Kalos, Michael D.

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Vedvick, Thomas S.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS

; FILE REFERENCE: 210121.544

; CURRENT APPLICATION NUMBER: US/09/930,125

; CURRENT FILING DATE: 2001-08-14

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 10

; LENGTH: 589

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-930-125-10

Query Match 100.0%; Score 54; DB 10; Length 589;
Best Local Similarity 100.0%; Pred. No. 0.03;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EYLVPOQGF 10
Db 355 EYLVPOQGF 364

RESULT 8

US-09-930-125-11

; Sequence 11, Application US/09930125

; Publication No. US20020193329A1

; GENERAL INFORMATION:

; APPLICANT: Hand-Zimmerman, Susan

; APPLICANT: Cheever, Martin A.

; APPLICANT: Foy, Teresa M.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Kalos, Michael D.

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Vedvick, Thomas S.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS

; FILE REFERENCE: 210121.544

; CURRENT APPLICATION NUMBER: US/09/930,125

; CURRENT FILING DATE: 2001-08-14

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 11

; LENGTH: 600

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-930-125-11

Query Match 100.0%; Score 54; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPOQGF 10
Db 366 EYLVPOQGF 375

RESULT 9

US-09-854-356-7

; Sequence 7, Application US/09854356

; Patent No. US2002017567A1

; GENERAL INFORMATION:

; APPLICANT: Cheever, Martin A.

; APPLICANT: Gheysen, Dirk

; APPLICANT: Corixa Corporation

; APPLICANT: SmithKline Beecham Biologicals S. A.

; TITLE OF INVENTION: HER-2/neu Fusion Proteins

; FILE REFERENCE: 014058-009810P

; CURRENT APPLICATION NUMBER: US/09/854,356

; CURRENT FILING DATE: 2001-05-09

; PRIOR APPLICATION NUMBER: US 09/493,480

; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: US 60/117,976

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn ver. 2.1

; SEQ ID NO 7

; LENGTH: 712

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: fusion protein

; OTHER INFORMATION: of ECD and delta PD of human HER-2/neu

US-09-854-356-7

Query Match 100.0%; Score 54; DB 10; Length 712;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DP 10062
20020177567

Qy 1 EYLVPOQGF 10
| | | | | | | |
Db 685 EYLVPOQGF 694

RESULT 10
US-09-854-356-6
; Sequence 6, Application US/09854356
; Patent No. US2002017567A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Cheysen, Dirk
; APPLICANT: Corixa Corporation
; APPLICANT: SmithKline Beecham Biologicals S. A.
; TITLE OF INVENTION: HER-2/neu Fusion Proteins
; FILE REFERENCE: 014058-009810PC
; CURRENT APPLICATION NUMBER: US/09/854,356
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US/09/493,480
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,976
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 919
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fusion protein
; OTHER INFORMATION: of ECD and PD of human HER-2/neu
US-09-854-356-6

Query Match 100.0%; Score 54; DB 10; Length 919;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPOQGF 10
| | | | | | | |
Db 685 EYLVPOQGF 694

RESULT 11
US-10-146-473-72
; Sequence 72, Application US/10146473
; Publication No. US2003010888A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146,473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 72
; LENGTH: 1253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-473-72

Query Match 100.0%; Score 54; DB 15; Length 1253;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPOQGF 10
| | | | | | | |

Db 1021 EYLVPOQGF 1030

RESULT 12
US-09-811-123-9
; Sequence 9, Application US/09811123
; Patent No. US2002001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall
; APPLICANT: Mark Sliwkowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-HERB
; FILE REFERENCE: ANTIBODY-MAYTANSINOID CONJUGATES
; CURRENT APPLICATION NUMBER: US/09/811,123
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-811-123-9

Query Match 100.0%; Score 54; DB 9; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPOQGF 10
| | | | | | | |
Db 1021 EYLVPOQGF 1030

RESULT 13
US-09-811-115-3
; Sequence 3, Application US/09811115
; Patent No. US20020035736A1
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT.034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-811-115-3

Query Match 100.0%; Score 54; DB 9; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPOQGF 10
| | | | | | | |
Db 1021 EYLVPOQGF 1030

RESULT 14
US-09-769-508-2
; Sequence 2, Application US/09769508
; Patent No. US2002015527A1
; GENERAL INFORMATION:

Db 1021 EYLVPPQGF 1030

Search completed: July 28, 2003, 17:14:58
Job time : 51 secs

APPLICANT: STUART, SUSAN G.
APPLICANT: MONAHAN, JOHN J.
APPLICANT: LANGTON, BEATRICE CLAUDIA
APPLICANT: HANCOCK, MIRIAM E.C.
APPLICANT: CHAO, LORRINE A.
APPLICANT: BLUFORD, PETER
TITLE OF INVENTION: C-ERBB-2 EXTERNAL DOMAIN: GP75
FILE REFERENCE: BEBIO-111-C1
CURRENT APPLICATION NUMBER: US/09/769,508
CURRENT FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 1255
TYPE: PRT
ORGANISM: Homo sapiens
US-09-769-508-2

Query Match 100.0%; Score 54; DB 10; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPPQGF 10
Db 1021 EYLVPPQGF 1030

RESULT 15
US-09-854-356-1
Sequence 1, Application US/09854356
Patent No. US20020177567A1
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Gheysen, Dirk
APPLICANT: Corixa Corporation
APPLICANT: SmithKline Beecham Biologicals S. A.
TITLE OF INVENTION: HER-2/neu Fusion Proteins
FILE REFERENCE: 014058-009810PC
CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,976
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1255
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human HER-2/neu protein
NAME/KEY: DOMAIN
LOCATION: (1)..(653)
OTHER INFORMATION: extracellular domain (ECD)
NAME/KEY: DOMAIN
LOCATION: (676)..(1255)
OTHER INFORMATION: intracellular domain (ICD)
NAME/KEY: DOMAIN
LOCATION: (990)..(1255)
OTHER INFORMATION: phosphorylation domain (PD)
NAME/KEY: DOMAIN
LOCATION: (990)..(1048)
OTHER INFORMATION: fragment of the phosphorylation domain, preferred
OTHER INFORMATION: portion (delta PD)
US-09-854-356-1

Query Match 100.0%; Score 54; DB 10; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPPQGF 10
|||||

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2003, 16:44:34 ; Search time 82 Seconds
(without alignments)
19.357 Million cell updates/sec

Title: US-09-930-125-3
Perfect score: 54
Sequence: 1 EEVLVPQGF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24:	/SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	10	AAE20480	Naturally processe
2	54	100.0	10	AAU77115	Human Her-2/neu im
3	54	100.0	59	AAU77115	Human Her-2/neu pr
4	54	100.0	59	AAU77115	Human Her-2/neu on
5	54	100.0	266	AAU77115	Human Her-2/neu pr
6	54	100.0	266	AAU77115	Human Her-2/neu on
7	54	100.0	293	AAU77115	Breast and ovarian
8	54	100.0	583	AAE20483	Human protein for
9	54	100.0	587	AAE20481	Human protein for

10	54	100.0	589	23	AAE20484	Human protein for
11	54	100.0	600	23	AAE20482	Human protein for
12	54	100.0	712	21	AAU77115	Human Her-2/neu fu
13	54	100.0	712	23	AAU77115	Her-2/neu extracel
14	54	100.0	919	21	AAU77115	Human Her-2/neu fu
15	54	100.0	919	23	AAU77115	Her-2/neu extracel
16	54	100.0	920	23	AAU77115	Mouse Her-2/neu ex
17	54	100.0	926	23	AAU77115	Mouse Her-2/neu ex
18	54	100.0	1200	21	AAU77115	Human Her-2/neu pr
19	54	100.0	1223	23	AAU77115	Human Her-2/neu pr
20	54	100.0	1223	23	AAU77115	Human breast cance
21	54	100.0	1255	17	AAU77115	HER-2/neu protein.
22	54	100.0	1255	20	AAU77115	Human Her-2/neu on
23	54	100.0	1255	21	AAU77115	Human Her-2/neu pr
24	54	100.0	1255	21	AAU77115	Amino acid sequenc
25	54	100.0	1255	22	AAU77115	Human heregulin 2
26	54	100.0	1255	22	AAU77115	Human tyrosine kin
27	54	100.0	1255	22	AAU77115	Human Her-2/neu pr
28	54	100.0	1255	22	AAU77115	HER2/neu amino aci
29	54	100.0	1255	23	AAU77115	HER2 transgene pla
30	54	100.0	1255	23	AAU77115	Human Her-2 protei
31	54	100.0	1255	23	AAU77115	Human Her-2 antigen
32	54	100.0	1255	23	AAU77115	Human Her-2 protei
33	54	100.0	1255	23	AAU77115	Human Her-2/neu pr
34	54	100.0	1255	23	AAU77115	Human Her-2/neu po
35	54	100.0	1255	23	AAU77115	Human Her-2 (Erbb2)
36	54	100.0	1255	24	AAU77115	Breast cancer asso
37	54	100.0	1255	24	AAU77115	Human Her-2/neu pro
38	54	100.0	1256	21	AAU77115	Rat HER-2/neu prot
39	54	100.0	1256	21	AAU77115	Mouse Her-2/neu pr
40	54	100.0	1256	22	AAU77115	Amino acid sequenc
41	54	100.0	1256	23	AAU77115	Rat Her-2/neu onco
42	54	100.0	1256	23	AAU77115	Sequence of c-erbB
43	54	100.0	1433	14	AAU77115	Inhibitor of TK of
44	50	92.6	11	14	AAU77115	EGF-R derived pept
45	50	92.6	13	16	AAU77115	

ALIGNMENTS

RESULT 1
AAE20480
ID AAE20480 standard; peptide; 10 AA.
XX
AC AAE20480;
XX
DT 01-JUL-2002 (first entry)
XX
DE Naturally processed HLA-B44-restricted epitope of human Her-2/neu.
XX
Human; Her-2/Neu protein; immune response; gene therapy; breast cancer;
human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200214503-A2.
XX
PD 21-FEB-2002.
XX
PF 14-AUG-2001; 2001WO-US41733.
XX
PR 14-AUG-2000; 2000US-225152P.
PR 28-SEP-2000; 2000US-236428P.
PR 21-FEB-2001; 2001US-270520P.
(CORI-) CORIXA CORP.
PI Hand-zimmermann S, Cheever MA, Foy TM, Lodes MJ, Kalos MD;
PI McNeill PD, Vedvick TS;
XX WPI; 2002-280758/32.
DR

PT Novel isolated Her-2/Neu polypeptide composition useful for therapy,
 PT prevention and diagnosis of cancer, preferably breast cancer
 XX
 PS Claim 2; Page 87; 129pp; English.
 XX
 CC The invention relates to an isolated Her-2/Neu polypeptide composition
 CC effective for eliciting an immune response. The invention is useful for
 CC eliciting an immune response in a patient, where the patient is human.
 CC Leukocyte antigen (HLA)-B44 positive or is affected with breast cancer.
 CC The composition is useful for the therapy and diagnosis of cancer,
 CC preferably breast cancer, in pharmaceutical compositions, e.g., vaccine
 CC and other compositions for the diagnosis, prevention and treatment of
 CC human malignancies, for stimulating and/or expanding T cells specific for
 CC Her-2/Neu polypeptide and for inhibiting the development of cancer in a
 CC patient. The invention is useful for stimulating a T cell response in a
 CC human patient, as probe or primer for nucleic acid hybridisation, to
 CC selectively form duplex molecules with complementary stretches of the
 CC entire Her-2/Neu gene or gene fragments of interest, to isolate a full
 CC length gene from a suitable library, and to direct expression of a
 CC polypeptide in appropriate host-cells. The composition is useful in
 CC prophylactic or therapeutic applications and for the treatment of cancer,
 CC preferably for the immunotherapy of breast cancer and other Her-2/Neu-
 CC associated malignancies. The invention is useful in gene therapy. The
 CC present sequence is naturally processed HLA-B44-restricted epitope of
 CC human Her-2/Neu protein.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 54; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0041;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EBYLVPQQGF 10
 Db |||||||||
 1 EBYLVPQQGF 10
 RESULT 2
 AAU77115
 ID AAU77115 standard; Peptide; 10 AA.
 AC
 AC AAU77115;
 DT
 DT 05-JUN-2002 (first entry)
 XX
 DE Human Her-2/Neu immunogenic epitope.
 XX
 KW Human; Her-2/Neu; cytostatic; haematological malignancy; CML;
 KW acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL;
 KW chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;
 KW Hodgkin's lymphoma; T cell therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200213847-A2.
 XX
 PD 21-FEB-2002.
 XX
 PF 13-AUG-2001; 2001WO-US25408.
 XX
 XX 14-AUG-2000; 2000US-0638280.
 PR 28-SEP-2000; 2000US-0675904.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Gaiger A, Cheever MA, Hand-zimmermann S;
 XX
 DR WPI; 2002-280741/32.
 XX
 XX Inhibiting haematological malignancy development by administering
 PT polypeptide comprising immunogenic portion of Her-2/Neu, polynucleotide
 PT encoding the polypeptide, or antigen presenting cells expressing the
 PT polypeptide

XX
 PS Claim 2; Page 49; 74pp; English.
 XX
 CC The invention relates to a method for inhibiting development of
 CC haematological malignancy in a patient by administering a polypeptide
 CC comprising an immunogenic portion of Her-2/Neu or a polynucleotide
 CC encoding the polypeptide. Antigen presenting cells that express the
 CC protein can also be administered. The sequences are used for inhibiting
 CC development of haematological malignancy such as acute myelogenous
 CC leukaemia (AML), chronic myelogenous leukaemia (CML), chronic lymphocytic
 CC leukaemia (CLL), MDS, myelomas, Hodgkin's lymphoma and non-Hodgkin's
 CC lymphoma. This sequence represents a human Her-2/Neu immunogenic epitope.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 54; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0041;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EBYLVPQQGF 10
 Db |||||||||
 1 EBYLVPQQGF 10
 RESULT 3
 AAB21202
 ID AAB21202 standard; protein; 59 AA.
 XX
 AC AAB21202;
 XX
 DT 12-JAN-2001 (first entry)
 XX
 DE Human HER-2/Neu protein phosphorylation domain partial sequence.
 XX
 KW Human; HER-2/Neu; oncogene; tyrosine kinase; cytostatic; vaccine;
 KW breast cancer; prostate cancer; ovarian cancer; lung cancer;
 KW colon cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200044899-A1.
 XX
 PD 03-AUG-2000.
 XX
 PF 28-JAN-2000; 2000WO-US02164.
 XX
 XX 29-JAN-1999; 99US-0117976.
 PR (CORI-) CORIXA CORP.
 PA (SMIK) SMITHKLINE BEECHAM.
 XX
 PI Cheever MA, Gheysen D;
 XX
 DR WPI; 2000-505976/45.
 XX
 PT HER-2/Neu extracellular domain/phosphorylation domain fusion proteins
 PT useful for vaccinating against breast, ovarian, colon, lung and
 PT prostate cancers -
 XX
 PS Claim 27; Fig 11; 128pp; English.
 XX
 CC The present sequence is a preferred portion of the phosphorylation domain
 CC of the HER-2/Neu protein. HER-2/Neu is a member of the tyrosine kinase
 CC family of receptor-like glycoproteins and shows homology to the epidermal
 CC growth factor receptor (EGFR). It probably plays a part in cell growth
 CC and/or differentiation. The HER-2/Neu gene is an oncogene. An HER-2/Neu
 CC fusion protein comprising a HER-2/Neu extracellular domain fused to a
 CC HER-2/Neu phosphorylation domain may be used to treat or prevent cancer
 CC by eliciting or enhancing an immune response to the HER-2/Neu protein. It
 CC may be used to treat malignancies such as breast, ovarian, colon, lung
 CC and prostate cancers, and may be used as an antigen to vaccinate against
 CC these neoplasias.

Tue Jul 29 09:32:16 2003

fusion protein can be used to remove tumour cells from a sample in order to inhibit the development of cancer in a patient.

CC Query Match 100.0%; Score 54; DB 21; Length 59;
 CC Best Local Similarity 100.0%; Pred. No. 0.023;
 CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 59 AA;
 XX Query Match 100.0%; Score 54; DB 23; Length 59;
 XX Best Local Similarity 100.0%; Pred. No. 0.023; 0; Indels 0; Gaps 0;
 XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLVPQGGF 10
 DB 32 EBYLVPQGGF 41

RESULT 4
 ID AAM51147 standard; Protein; 59 AA.
 XX AAM51147;
 XX 17-JUN-2002 (first entry)
 XX Human Her-2/neu oncoprotein phosphorylation domain fragment.
 DE Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;
 KW tyrosine kinase; receptor; c-erbB2; gene therapy.
 KW Homo sapiens.
 OS WO200212341-A2.
 PN 14-FEB-2002.
 XX 03-AUG-2001; 2001WO-US24283.
 XX 03-AUG-2000; 2000US-0632507.
 XX (CORI-) CORIXA CORP.
 XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX Cheever MA, Gheysen D;
 XX WPI; 2002-241743/29.
 XX Her-2/neu fusion protein for treating or preventing cancer by eliciting
 PT or enhancing an immune response to the protein, has Her-2/neu
 PT extracellular domain fused to Her-2/neu intracellular or
 PT phosphorylation domain
 XX Disclosure; Fig 11; 141pp; English.

XX The present sequence is that of a fragment (DeltaAPP) of the
 CC phosphorylation domain of human Her-2/neu (p185 glycoprotein,
 CC c-erbB2), an oncogenic self-protein and target for anti-cancer
 CC vaccines. The Her-2/neu gene is amplified and p185 is
 CC overexpressed in breast, ovarian, colon, lung and prostate cancer.
 CC Her-2/neu (see AAM51143) is a member of the tyrosine kinase family
 CC of receptor-like glycoproteins. It comprises an extracellular
 CC domain with homology to the epidermal growth factor receptor
 CC (EGFR), a highly hydrophobic transmembrane domain and a C-terminal
 CC intracellular domain that also shows homology to EGFR. Its
 CC overexpression correlates with a poor prognosis in breast and
 CC ovarian cancers. The invention provides Her-2/neu fusion
 CC proteins, nucleic acids encoding them, viral vectors, and vaccines
 CC comprising the fusion proteins or nucleic acid molecules. In
 CC preferred fusion proteins, the extracellular domain of a Her-2/neu
 CC protein is fused to a Her-2/neu intracellular domain or
 CC phosphorylation domain (or the DeltaAPP fragment). An immune
 CC response to Her-2/neu protein is elicited or enhanced by
 CC administering the fusion protein in the form of a vaccine, or by
 CC administering cells of an animal *ex vivo* with a nucleic acid
 CC encoding the fusion protein, and delivering the transfected cells
 CC to the animal. The fusion proteins, nucleic acids, and isolated
 CC specific T-cells are useful for inhibiting the development of a
 CC cancer, especially breast, ovarian, colon, lung or prostate cancer
 CC in a patient. T cells that specifically react with a Her-2/neu

QY 1 EBYLVPQGGF 10
 DB 32 EBYLVPQGGF 41

RESULT 5
 ID AAB21201 standard; protein; 266 AA.
 XX AAB21201;
 XX 12-JAN-2001 (first entry)
 XX Human HER-2/neu protein phosphorylation domain.
 DE Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
 KW breast cancer; prostate cancer; ovarian cancer; lung cancer;
 KW colon cancer.
 OS Homo sapiens.
 XX WO200044899-A1.
 XX 03-AUG-2000.
 XX 28-JAN-2000; 2000WO-US02164.
 XX 29-JAN-1999; 99US-0117976.
 XX (CORI-) CORIXA CORP.
 XX (SMIK) SMITHKLINE BEECHAM.
 XX Cheever MA, Gheysen D;
 XX WPI; 2000-505976/45.
 XX HER-2/neu extracellular domain/phosphorylation domain fusion proteins
 PT useful for vaccinating against breast, ovarian, colon, lung and
 PT prostate cancers
 XX Claim 2; Fig 10; 128pp; English.

XX The present sequence is the phosphorylation domain of the HER-2/neu
 CC protein. HER-2/neu is a member of the tyrosine kinase family of
 CC receptor-like glycoproteins and shows homology to the epidermal growth
 CC factor receptor (EGFR). It probably plays a part in cell growth and/or
 CC differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion
 CC protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu
 CC phosphorylation domain may be used to treat or prevent cancer by
 CC eliciting or enhancing an immune response to the HER-2/neu protein. It
 CC may be used to treat malignancies such as breast, ovarian, colon, lung
 CC and prostate cancers, and may be used as an antigen to vaccinate against
 CC these neoplasias.

XX SQ Sequence 266 AA;
 XX Query Match 100.0%; Score 54; DB 21; Length 266;
 XX Best Local Similarity 100.0%; Pred. No. 0.1;
 XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLVPQGGF 10
 DB 32 EBYLVPQGGF 41

RESULT 6
 AAM51146
 ID AAM51146 standard; Protein; 266 AA.
 XX
 AC AAM51146;
 XX
 DT 17-JUN-2002 (first entry)
 XX
 DE Human Her-2/neu oncoprotein phosphorylation domain.
 XX
 KW Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;
 XX tyrosine kinase; receptor; c-erbB2; gene therapy.
 OS Homo sapiens.
 XX
 PN WO200212341-A2.
 XX
 PD 14-FEB-2002.
 XX
 PF 03-AUG-2001; 2001WO-US24283.
 XX
 PR 03-AUG-2000; 2000US-0632507.
 XX
 PA (CORI-) CORIXA CORP.
 XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 PI Cheever MA, Gheysen D;
 XX
 DR WPI; 2002-241743/29.
 XX
 PT Her-2/neu fusion protein for treating or preventing cancer by eliciting
 PT or enhancing an immune response to the protein, has Her-2/neu
 PT extracellular domain fused to Her-2/neu intracellular or
 PT phosphorylation domain
 XX
 PS Claim 2; Fig 10; 141pp; English.
 XX
 CC The present sequence is that of the phosphorylation domain of
 CC human Her-2/neu (p185 glycoprotein or c-erbB2), an oncogenic
 CC self-protein and target for anti-cancer vaccines. The Her-2/neu
 CC gene is amplified and p185 is overexpressed in a variety of cancers,
 CC including breast, ovarian, colon, lung and prostate cancer.
 CC Her-2/neu (see AAM51143) is a member of the tyrosine kinase family
 CC of receptor-like glycoproteins. It comprises an extracellular
 CC domain with homology to the epidermal growth factor receptor
 CC (EGFR), a highly hydrophobic transmembrane domain and a C-terminal
 CC intracellular domain that also shows homology to EGFR. Its
 CC overexpression correlates with a poor prognosis in breast and
 CC ovarian cancers. The invention provides Her-2/neu fusion
 CC proteins, nucleic acids encoding them, viral vectors, and vaccines
 CC comprising the fusion proteins or nucleic acid molecules. In
 CC preferred fusion proteins, the extracellular domain of a Her-2/neu
 CC protein is fused to a Her-2/neu intracellular domain or
 CC phosphorylation domain (or its DeltaCD fragment). An immune
 CC response to Her-2/neu protein is elicited or enhanced by
 CC administering the fusion protein in the form of a vaccine, or by
 CC transfecting cells of an animal *ex vivo* with a nucleic acid
 CC encoding the fusion protein, and delivering the transfected cells
 CC to the animal. The fusion proteins, nucleic acids, and isolated
 CC specific T-cells are useful for inhibiting the development of a
 CC cancer, especially breast, ovarian, colon, lung or prostate cancer
 CC in a patient. T cells that specifically react with a Her-2/neu
 CC fusion protein can be used to remove tumour cells from a sample in
 CC order to inhibit the development of cancer in a patient.
 XX
 SQ Sequence 266 AA;
 Query Match 100.0%; Score 54; DB 23; Length 266;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EYLVPPQGF 10

Db 32 EYLVPPQGF 41
 RESULT 7
 AAB58875
 ID AAB58875 standard; Protein; 293 AA.
 XX
 AC AAB58875;
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 583.
 XX
 KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
 KW neutropic; neuroprotective; antiviral; antiallergic; hepatotropic;
 KW antidiabetic; antiinflammatory; antiulcer; vulnery; anticonvulsant;
 KW antibacterial; antifungal; antiparasitic; cardiac; immune disorder;
 KW Addison's disease; allergy; autoimmune haemolytic anaemia;
 KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
 KW cardiovascular disorder; wound healing; neurological disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200055173-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000WO-US05881.
 XX
 PR 12-MAR-1999; 99US-0124270.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI; 2000-611515/58.
 XX
 DR N-PSDB; AAF21778.
 XX
 PT New human breast and ovarian cancer associated gene sequences and the
 PT polypeptides encoded by these genes, useful in the prevention,
 PT treatment and diagnosis of cancer, immune disorders, cardiovascular
 PT disorders and neurological diseases
 XX
 PS Claim 11; Page 1019-1020; 1299pp; English.
 XX
 CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
 CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
 CC associated with breast and ovarian cancer. Included in the invention are
 CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
 CC isolation and characterisation of the DNA and protein sequences of the
 CC invention. The breast and ovarian cancer associated DNA, protein, agonist
 CC or antagonist sequences exhibit cytostatic; immunosuppressive;
 CC neutropic; neuroprotective; antiviral; antiallergic; hepatotropic;
 CC antidiabetic; antiinflammatory; antiulcer; vulnery; anticonvulsant;
 CC antibacterial; antifungal; antiparasitic and cardiac activity. The
 CC polynucleotide and protein sequences are used in the diagnosis of cancer,
 CC particularly breast and ovarian cancer. The nucleic acid sequences,
 CC proteins, agonists and antagonists may also be used in the diagnosis,
 CC prevention and treatment of immune disorders e.g. Addison's disease,
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
 CC arthritis and ulcerative colitis; cardiovascular disorders such as
 CC myocardial ischaemia; wound healing; neurological diseases such as
 CC cerebral anoxia and epilepsy; and infectious diseases.
 XX
 SQ Sequence 293 AA;
 Query Match 100.0%; Score 54; DB 21; Length 293;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBYLVPQOGF 10
 Db 105 EBYLVPQOGF 114

RESULT 8
 AAE20483
 ID AAE20483 standard; Protein; 583 AA.
 AC AAE20483;
 XX
 DT 01-JUL-2002 (first entry)
 XX

Human protein for the clone HICD_native_coding_region.

Human; Her-2/Neu protein; immune response; gene therapy; breast cancer;
 human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.

OS Homo sapiens.

Key Location/Qualifiers
 FH Misc-difference 581..583
 FT /note= "Encoded by GTGTAATGACTC"

XX WO200214503-A2.

PN 21-FEB-2002.

XX 14-AUG-2001; 2001WO-US41733.

XX 14-AUG-2000; 2000US-225152P.

PR 28-SEP-2000; 2000US-236428P.

PR 21-FEB-2001; 2001US-270520P.

XX (CORI-) CORIXA CORP.

XX Hand-zimmermann S, Cheever MA, Foy TM, Lodes MJ, Kalos MD;

PI McNeill PD, Vedvick TS;

PI WPI; 2002-280758/32.

DR N-PSDB; AAD32746.

XX Novel isolated Her-2/Neu polypeptide composition useful for therapy,

PT prevention and diagnosis of cancer, preferably breast cancer

XX Example 5; Page 121-122; 129pp; English.

PS The invention relates to an isolated Her-2/Neu polypeptide composition

XX effective for eliciting an immune response. The invention is useful for

CC eliciting an immune response in a patient, where the patient is human

CC leukocyte antigen (HLA)-B44 positive or is affected with breast cancer.

CC The composition is useful for the therapy and diagnosis of cancer.

CC and other compositions for the diagnosis, prevention and treatment of

CC human malignancies, for stimulating and/or expanding T cells specific for

CC Her-2/Neu polypeptide and for inhibiting the development of cancer in a

CC patient. The invention is useful for stimulating a T cell response in a

CC selectively form duplex molecules with complementary stretches of the

CC entire Her-2/Neu gene or gene fragments of interest, to isolate a full

CC length gene from a suitable library, and to direct expression of a

CC polypeptide in appropriate host cells. The composition is useful in

CC prophylactic or therapeutic applications and for the treatment of cancer,

CC preferably for the immunotherapy of breast cancer and other Her-2/Neu-

CC associated malignancies. The invention is useful in gene therapy. The

CC present sequence is human protein for the clone HICD_native_coding_

XX region.

SQ Sequence 583 AA;

Query Match

Best Local Similarity 100.0%; Score 54; DB 23; Length 583;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBYLVPQOGF 10
 Db 347 EBYLVPQOGF 356

RESULT 9
 AAE20481
 ID AAE20481 standard; Protein; 587 AA.
 AC AAE20481;
 XX
 DT 01-JUL-2002 (first entry)
 XX

Human protein for the clone HICD_CT_His_coding_region.

Human; Her-2/Neu protein; immune response; gene therapy; breast cancer;
 human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.

OS Homo sapiens.

PN WO200214503-A2.

XX 21-FEB-2002.

PD 14-AUG-2001; 2001WO-US41733.

XX 14-AUG-2000; 2000US-225152P.

PR 28-SEP-2000; 2000US-236428P.

PR 21-FEB-2001; 2001US-270520P.

XX (CORI-) CORIXA CORP.

XX Hand-zimmermann S, Cheever MA, Foy TM, Lodes MJ, Kalos MD;

PI McNeill PD, Vedvick TS;

PI WPI; 2002-280758/32.

DR N-PSDB; AAD32744.

XX Novel isolated Her-2/Neu polypeptide composition useful for therapy,

PT prevention and diagnosis of cancer, preferably breast cancer

XX Example 5; Page 120-121; 129pp; English.

PS The invention relates to an isolated Her-2/Neu polypeptide composition

XX effective for eliciting an immune response. The invention is useful for

CC eliciting an immune response in a patient, where the patient is human

CC leukocyte antigen (HLA)-B44 positive or is affected with breast cancer.

CC The composition is useful for the therapy and diagnosis of cancer,

CC and other compositions for the diagnosis, prevention and treatment of

CC human malignancies, for stimulating and/or expanding T cells specific for

CC Her-2/Neu polypeptide and for inhibiting the development of cancer in a

CC patient. The invention is useful for stimulating a T cell response in a

CC selectively form duplex molecules with complementary stretches of the

CC entire Her-2/Neu gene or gene fragments of interest, to isolate a full

CC length gene from a suitable library, and to direct expression of a

CC polypeptide in appropriate host cells. The composition is useful in

CC prophylactic or therapeutic applications and for the treatment of cancer,

CC preferably for the immunotherapy of breast cancer and other Her-2/Neu-

CC associated malignancies. The invention is useful in gene therapy. The

CC present sequence is human protein for the clone HICD_CT_His_coding_

XX region.

SQ Sequence 587 AA;

Query Match

Best Local Similarity 100.0%; Score 54; DB 23; Length 587;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBYLVPQOGF 10

Db 347 EBYLVPQOGF 356

RESULT 12

AAB21204
ID AAB21204 standard; protein; 712 AA.

XX
AC AAB21204;

XX
DT 12-JAN-2001 (first entry)

XX
DE Human HER-2/neu fusion protein.

XX
KW Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
KW breast cancer; prostate cancer; ovarian cancer; lung cancer;
KW colon cancer; fusion protein.

XX
OS Homo sapiens.

XX
OS Synthetic.

XX
PN WO200044899-A1.

XX
XX 03-AUG-2000.

XX
PF 28-JAN-2000; 2000WO-US02164.

XX
PR 29-JAN-1999; 99US-0117976.

XX
PA (CORI-) CORIXA CORP.

XX
PA (SMIK) SMITHKLINE BEECHAM.

XX
PI Cheever MA, Gheysen D;

XX
XX WPI; 2000-505976/45.

XX
PT HER-2/neu extracellular domain/phosphorylation domain fusion proteins
PT useful for vaccinating against breast, ovarian, colon, lung and
PT prostate cancers

XX
PS Claim 27; Fig 13; 128pp; English.

XX
CC The present sequence is a fusion protein comprising the extracellular
CC domain and a preferred portion of the phosphorylation domain of the human
CC HER-2/neu protein. HER-2/neu is a member of the tyrosine kinase family of
CC receptor-like glycoproteins and shows homology to the epidermal growth
CC factor receptor (EGFR). It probably plays a part in cell growth and/or
CC differentiation. The HER-2/neu gene is an oncogene. HER-2/neu fusion
CC proteins may be used to treat or prevent cancer by eliciting or enhancing
CC an immune response to the HER-2/neu protein. They may be used to treat
CC malignancies such as breast, ovarian, colon, lung and prostate cancers,
CC and may be used as an antigen to vaccinate against these neoplasias.

XX
SQ Sequence 712 AA;

Query Match 100.0%; Score 54; DB 21; Length 712;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEYLVPPQGF 10
|||||
Db 685 EEYLVPPQGF 694

RESULT 13

AAM51149
ID AAM51149 standard; Protein; 712 AA.

XX
AC AAM51149;

XX
DT 17-JUN-2002 (first entry)

XX
DE Her-2/neu extracellular domain-delta-phosphorylation domain fusion.

XX
KW Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;

XX
KW tyrosine kinase; receptor; c-erbB2; gene therapy.

OS Homo sapiens.

XX
FH Key Location/Qualifiers

FT Domain 1..653

FT /note= "extracellular domain"

FT Domain 654..712

FT /note= "phosphorylation domain fragment"

XX
PN WO200212341-A2.

XX
PD 14-FEB-2002.

XX
PF 03-AUG-2001; 2001WO-US24283.

XX
PR 03-AUG-2000; 2000US-0632507.

XX
PA (CORI-) CORIXA CORP.

XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX
PI Cheever MA, Gheysen D;

XX
XX WPI; 2002-241743/29.

XX
PT Her-2/neu fusion protein for treating or preventing cancer by eliciting
PT or enhancing an immune response to the protein, has Her-2/neu
PT extracellular domain fused to Her-2/neu intracellular or
PT phosphorylation domain

XX
PS Claim 37; Fig 13; 141pp; English.

XX
CC The present sequence is that of a fusion protein between the
CC extracellular domain and a fragment (DeltapD) of the phosphorylation
CC domain of human Her-2/neu (see AAM51143), an oncogenic self-protein
CC and target for anti-cancer vaccines. The fusion protein can be
CC obtained by recombinant DNA methods. Her-2/neu overexpression
CC correlates with a poor prognosis in breast and ovarian cancers.
CC The invention provides Her-2/neu fusion proteins, nucleic acids
CC encoding them, viral vectors, and vaccines comprising the fusion
CC proteins or nucleic acid molecules. In preferred fusion proteins,
CC the extracellular domain of Her-2/neu is fused to a Her-2/neu
CC intracellular domain or phosphorylation domain (or its DeltapD
CC fragment). An immune response to Her-2/neu protein is elicited or
CC enhanced by administering the fusion protein in the form of a vaccine,
CC or by transfecting cells of an animal ex vivo with a nucleic acid
CC encoding the fusion protein, and delivering the transfected cells
CC to the animal. The fusion proteins, nucleic acids, and isolated
CC specific T-cells are useful for inhibiting the development of a
CC cancer, especially breast, ovarian, colon, lung or prostate cancer
CC in a patient. T cells that specifically react with a Her-2/neu
CC fusion protein can be used to remove tumour cells from a sample in
CC order to inhibit the development of cancer in a patient.

XX
SQ Sequence 712 AA;

Query Match 100.0%; Score 54; DB 23; Length 712;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEYLVPPQGF 10
|||||
Db 685 EEYLVPPQGF 694

RESULT 14

AAB21203

ID AAB21203 standard; protein; 919 AA.

XX
AC AAB21203;

XX
DT 12-JAN-2001 (first entry)

XX
DE Human HER-2/neu fusion protein.

KW Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
 KW breast cancer; prostate cancer; ovarian cancer; lung cancer;
 KW colon cancer; fusion protein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO200044899-A1.
 XX
 PN 03-AUG-2000.
 PD
 XX 28-JAN-2000; 2000WO-US02164.
 PF 29-JAN-1999; 99US-0117976.
 XX
 XX (CORI-) CORIXA CORP.
 PA (SMIK) SMITHKLINE BEECHAM.
 PA
 XX Cheever MA, Gheysen D;
 PI
 XX WPI; 2000-505976/45.
 DR
 XX HER-2/neu extracellular domain/phosphorylation domain fusion proteins
 PT useful for vaccinating against breast, ovarian, colon, lung and
 PT prostate cancers
 XX
 PS Claim 2; Fig 12; 128pp; English.
 XX
 CC The present sequence is a fusion protein comprising the extracellular
 CC domain and the phosphorylation domain of the human HER-2/neu protein.
 CC HER-2/neu is a member of the tyrosine kinase family of receptor-like
 CC glycoproteins and shows homology to the epidermal growth factor receptor
 CC (EGFR). It probably plays a part in cell growth and/or differentiation.
 CC The HER-2/neu gene is an oncogene. HER-2/neu fusion proteins may be used
 CC to treat or prevent cancer by eliciting or enhancing an immune response
 CC to the HER-2/neu protein. They may be used to treat malignancies such as
 CC breast, ovarian, colon, lung and prostate cancers, and may be used as an
 CC antigen to vaccinate against these neoplasias.
 XX
 SQ Sequence 919 AA;
 Query Match 100.0%; Score 54; DB 21; Length 919;
 Best Local Similarity 100.0%; Pred. No. 0.34;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EYLVPPQGGF 10
 Db |||||
 685 EYLVPPQGGF 694
 RESULT 15
 AAM51148
 ID AAM51148 standard; Protein; 919 AA.
 XX
 AC AAM51148;
 XX
 DT 17-JUN-2002 (first entry)
 DE
 XX Her-2/neu extracellular domain-phosphorylation domain fusion.
 KW Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;
 KW tyrosine kinase; receptor; c-erbB2; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Domain 1..653
 FT /note= "extracellular domain"
 FT Domain 654..919
 FT /note= "phosphorylation domain"
 XX
 PN WO200212341-A2.
 XX

PD 14-FEB-2002.
 XX
 PF 03-AUG-2001; 2001WO-US24283.
 XX
 PR 03-AUG-2000; 2000US-0632507.
 XX
 PA (CORI-) CORIXA CORP.
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 PI Cheever MA, Gheysen D;
 XX
 DR WPI; 2002-241743/29.
 XX
 XX Her-2/neu fusion protein for treating or preventing cancer by eliciting
 PT or enhancing an immune response to the protein, has Her-2/neu
 PT extracellular domain fused to Her-2/neu intracellular or
 PT phosphorylation domain
 XX
 PS Claim 2; Fig 12; 141pp; English.
 XX

CC The present sequence is that of a fusion protein between the
 CC extracellular domain and phosphorylation domain of human Her-2/neu
 CC (see AAM51143), an oncogenic self-protein and target for anti-cancer
 CC vaccines. The fusion protein can be obtained by recombinant DNA
 CC methods. Her-2/neu overexpression correlates with a poor prognosis
 CC in breast and ovarian cancers. The invention provides Her-2/neu
 CC fusion proteins, nucleic acids encoding them, viral vectors, and
 CC vaccines comprising the fusion proteins or nucleic acid molecules.
 CC In preferred fusion proteins, the extracellular domain of a
 CC Her-2/neu protein is fused to a Her-2/neu intracellular domain or
 CC phosphorylation domain (or its DeltapD fragment). An immune
 CC response to Her-2/neu protein is elicited or enhanced by
 CC administering the fusion protein in the form of a vaccine, or by
 CC transfecting cells of an animal ex vivo with a nucleic acid
 CC encoding the fusion protein, and delivering the transfected cells
 CC to the animal. The fusion proteins, nucleic acids, and isolated
 CC specific T-cells are useful for inhibiting the development of a
 CC cancer, especially breast, ovarian, colon, lung or prostate cancer
 CC in a patient. T cells that specifically react with a Her-2/neu
 CC fusion protein can be used to remove tumour cells from a sample in
 CC order to inhibit the development of cancer in a patient.
 XX
 SQ Sequence 919 AA;

Query Match 100.0%; Score 54; DB 23; Length 919;
 Best Local Similarity 100.0%; Pred. No. 0.34;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPPQGGF 10
 Db |||||
 685 EYLVPPQGGF 694

Search completed: July 28, 2003, 17:03:42
 Job time : 83 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2003, 17:00:20 ; Search time 96 Seconds
(without alignments)
26.880 Million cell updates/sec

Title: US-09-930-125-3
Perfect score: 54
Sequence: 1 EYLVPQGF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriophage.*
- 17: sp_archaeal.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	367	11 Q8R2X1	Q8R2X1 mus musculus
2	54	100.0	412	4 Q8WV0	Q8WV0 homo sapien
3	54	100.0	881	11 Q8C0E7	Q8C0E7 mus musculus
4	54	100.0	1259	6 O18735	O18735 canis famil
5	54	100.0	1259	11 Q8K3E9	Q8K3E9 rattus norv
6	51	94.4	1209	6 Q8M1L8	Q8M1L8 sus scrofa
7	50	92.6	1209	11 Q9QX70	Q9QX70 rattus norv
8	47	87.0	1210	11 Q9EP98	Q9EP98 mus musculus
9	46	85.2	545	15 Q85468	Q85468 avian eryth
10	46	85.2	567	15 Q86714	Q86714 avian rous-
11	46	85.2	729	15 Q86712	Q86712 avian eryth
12	46	85.2	962	15 Q64895	Q64895 avian eryth
13	40	74.1	876	2 Q32739	Q32739 clostridium
14	40	74.1	876	2 Q9KH41	Q9KH41 clostridium
15	38	70.4	910	12 Q9Q915	Q9Q915 avian adeno
16	37	68.5	75	11 Q88460	Q88460 mus musculus

17	37	68.5	428	16 Q92BW2	Q92BW2 listeria in
18	37	68.5	428	16 Q8Y797	Q8Y797 listeria mo
19	37	68.5	539	3 Q01143	Q01143 magnaporthe
20	37	68.5	694	5 Q9UB16	Q9UB16 caenorhabdi
21	37	68.5	753	5 Q9XZD4	Q9XZD4 caenorhabdi
22	37	68.5	861	5 Q8ML27	Q8ML27 drosophila
23	37	68.5	1137	13 Q9W6F6	Q9W6F6 gallus gall
24	36	66.7	173	2 Q8GLE5	Q8GLE5 xenorhabdus
25	36	66.7	332	4 Q9HAA2	Q9HAA2 homo sapien
26	36	66.7	332	4 Q96CY5	Q96CY5 homo sapien
27	36	66.7	375	4 Q8WVN8	Q8WVN8 homo sapien
28	36	66.7	422	5 Q9VKT8	Q9VKT8 drosophila
29	36	66.7	436	17 Q97Z48	Q97Z48 xenopus lae
30	36	66.7	1730	13 Q8UVY7	Q8UVY7 xenopus lae
31	36	66.7	2259	11 Q921C2	Q921C2 mus musculu
32	36	66.7	2304	11 Q921C3	Q921C3 mus musculu
33	36	66.7	3906	2 Q8G987	Q8G987 planktothri
34	35	64.8	209	3 Q94461	Q94461 schizosacch
35	35	64.8	322	16 Q8DD55	Q8DD55 vibrio vuln
36	35	64.8	365	16 Q987M5	Q987M5 rhizobium l
37	35	64.8	481	13 Q8JFP7	Q8JFP7 brachydanio
38	35	64.8	516	3 Q9Y7E1	Q9Y7E1 aspergillus
39	35	64.8	686	11 Q91VG9	Q91VG9 mus musculu
40	35	64.8	686	11 Q9WVJ6	Q9WVJ6 rattus norv
41	35	64.8	686	11 Q8C217	Q8C217 mus musculu
42	35	64.8	852	2 Q9AM64	Q9AM64 acinetobact
43	35	64.8	917	10 Q94C76	Q94C76 arabidopsis
44	35	64.8	1448	5 Q8T683	Q8T683 dictyostell
45	35	64.8	2269	4 Q96QG9	Q96QG9 homo sapien

ALIGNMENTS

RESULT 1	Q8R2X1	PRELIMINARY;	PRT;	367 AA.
ID	Q8R2X1	PRELIMINARY;	PRT;	367 AA.
AC	Q8R2X1			
DT	01-JUN-2002 (TREMBLrel. 21, Created)			
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Hypothetical 40.2 kDa protein.			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Strausberg R.			
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC027080; AAH27080.1; -			
DR	InterPro; IPR000719; Prot_kinase.			
DR	InterPro; IPR004019; YLP_motif.			
DR	Pfam; PF00069; pkinase; 1.			
DR	Pfam; PF02757; YLP; 2.			
DR	ProDom; PD000001; Prot_kinase; 1.			
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.			
KW	Hypothetical protein; ATP-binding; Transferase.			
SQ	SEQUENCE 367 AA; 40163 MW; OBE03395F9E101B0 CRC64;			

Query Match 100.0%; Score 54; DB 11; Length 367;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches: 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	EYLVPQGF 10
Db	133	EYLVPQGF 142

RESULT 2	Q8WV0	PRELIMINARY;	PRT;	412 AA.
ID	Q8WV0	PRELIMINARY;	PRT;	412 AA.
AC	Q8WV0			

```

DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN PP3659.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,
RA Wan D.F., Gu J.R.;
RT "Novel human cDNA clones with function of inhibiting cancer cell
RT growth.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF318349; AAL55856.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR004019; YLP_motif.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF02757; YLP; 2.
DR PRINTS; PR00109; TYRKINASE.
DR PROSITE; PS00001; Prot_kinase; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR Hypothetical protein; ATP-binding; Kinase; Transferase;
KW Tyrosine-protein kinase.
SQ SEQUENCE 412 AA; 44702 MW; 034397FF3F27D2BC CRC64;

Query Match 100.0%; Score 54; DB 4; Length 412;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEYLVPOQGF 10
DB 133 EEYLVPOQGF 142

RESULT 3
ID Q8C0E7 PRELIMINARY; PRT; 881 AA.
AC Q8C0E7;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE V-erb-b2 erythroblastic leukemia viral oncogene homolog 2
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK031542; BAC27442.1; -.
FT NON_TER 1
SQ SEQUENCE 881 AA; 97501 MW; 5D5042BE9F8F0836 CRC64;

Query Match 100.0%; Score 54; DB 11; Length 881;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEYLVPOQGF 10
DB 647 EEYLVPOQGF .656

RESULT 4
ID Q18735 PRELIMINARY; PRT; 1259 AA.
AC Q18735;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE ErB-2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Yokota H.;
RT "cDNA cloning of erbB-2 from canine mammary gland.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB008451; BAA23127.1; -.
DR HSP; P11362; IFGK.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000494; EGFR_L_domain.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin-repeat.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR004019; YLP_motif.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR Pfam; PF02757; YLP; 2.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SMO0261; FU; 3.
DR SMART; SMO0219; TyKc; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
SQ SEQUENCE 1259 AA; 137989 MW; E37364D49C4ACD46 CRC64;

Query Match 100.0%; Score 54; DB 6; Length 1259;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEYLVPOQGF 10
DB 1020 EEYLVPOQGF 1029

RESULT 5
ID Q8K3F9 PRELIMINARY; PRT; 1259 AA.
AC Q8K3F9;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Neu protooncoprotein
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BDIX;
RA Watson P.A., Kim K., Chen K.-S., Gould M.N.;
RT "Androgen-Dependent Mammary Carcinogenesis in Rats Transgenic for the
RT Neu Proto-Oncogene.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY116182; RAM50093.1; -.
DR InterPro; IPR002048; EF-hand.

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DR InterPro; IPR000494; EGFR_L_domain.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 1259 AA; 139102 MW; B724BD5CC3AE953 CRC64;

Query Match 100.08; Score 54; DB 11; Length 1259;
Best Local Similarity 100.08; Pred. No. 0.088;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBYLVPQOGF 10
|||||
Db 1025 EBYLVPQOGF 1034

RESULT 6
Q8MIL8 PRELIMINARY; PRT; 1209 AA.
AC Q8MIL8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Epidermal growth factor receptor.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim J.G., Vallet J.L., Nonneman D., Christenson R.K.;
RT "Characterization of uterine epidermal growth factor receptor
expression during the estrous cycle and early pregnancy in pigs."
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY117054; AAM77472.1;
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR000494; EGFR_L_domain.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Receptor; Transferase.
SQ SEQUENCE 1209 AA; 133531 MW; 268E3FB11E36F90F CRC64;

Query Match 94.4%; Score 51; DB 6; Length 1209;
Best Local Similarity 90.0%; Pred. No. 0.26;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBYLVPQOGF 10
|||||

Db 1015 DEYLVPQOGF 1024

RESULT 8
Q9EP98 PRELIMINARY; PRT; 1210 AA.
AC Q9EP98;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Epidermal growth factor receptor isoform 1.
EGFR.

Db 1014 DEYLVPQOGF 1023

RESULT 7
Q9QX70 PRELIMINARY; PRT; 1209 AA.
AC Q9QX70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Epidermal growth factor receptor.
EGFR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fisher; TISSUE=Liver;
RX MEDLINE=90258888; PubMed=2342466;
RA Petch L.A., Harris J., Raymond V.W., Blasband A.J., Lee D.C.,
RA Earp H.S.;
RT "A truncated, secreted form of the epidermal growth factor receptor-is
RT encoded by an alternatively spliced transcript in normal rat tissue."
RL Mol. Cell. Biol. 10:2973-2982(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Fisher; TISSUE=Liver;
RA Petch L.A.;
RL Submitted (NOV-1991) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Fisher; TISSUE=Liver;
RA Guttridge K., Dawson T.L., Earp H.S.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; M37394; AAF14008.1;
DR HSP; P11362; LFEGK.
DR InterPro; IPR000494; EGFR_L_domain.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin-repeat.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00261; FU; 3.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Kinase; Receptor; Transferase; Tyrosine-protein kinase.
SQ SEQUENCE 1209 AA; 134891 MW; 96FEF7F6CC1B7773 CRC64;

Query Match 92.6%; Score 50; DB 11; Length 1209;
Best Local Similarity 80.0%; Pred. No. 0.41;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBYLVPQOGF 10
|||||
Db 1015 DEYLVPQOGF 1024

RESULT 8
Q9EP98 PRELIMINARY; PRT; 1210 AA.
AC Q9EP98;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Epidermal growth factor receptor isoform 1.
EGFR.

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RP SEQUENCE FROM N.A.
RR MEDLINE=86217326; PubMed=2897102;
RX Scotting P., Vennstrom B., Jansen M., Graf T., Beug H., Haymann M.J.;
RA "Common site of mutation in the erbB gene of avian erythroblastosis
RT virus mutants that are temperature sensitive for transformation.";
RL Oncogene res. 1:265-278(1987).
DR EMBL; X06943; CAA30024.1; -.
DR HSSP; P11362; LFCK
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SW00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR ATP-binding; Kinase; Transferrase; Tyrosine-protein kinase.
KW ATP-binding; Kinase; Transferrase; Tyrosine-protein kinase.
SQ SEQUENCE 545 AA; 60899 MW; 140DCE8CCA0F8AF4 CRC64;

Query Match 85.2%; Score 46; DB 15; Length 545;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEXYLPQOGF 10
Db 439 DEYLPHQGF 448

RESULT 10
Q86714 PRELIMINARY; PRT; 567 AA.
ID Q86714;
AC Q86714;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NAR-2003 (TREMBLrel. 23, Last annotation update)
DE v-erbB protein (Fragment).
GN v-ERBB.
OS Avian rous-associated virus type 1.
OC Viruses; Retrov. viruses; Retroviridae; Alpharetrovirus.
OX NCBI_Taxid=11950;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94203659; PubMed=8152791;
RA Vennstrom B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V.,
RA Johnson A., Beug H.;
RA "Retroviral capture of c-erbB proto-oncogene sequences: rapid
RT evolution of distinct viral genomes carrying mutant v-erbB genes with
RT different transforming capacities.";
RL Oncogene 9:1307-1320(1994).
DR EMBL; S69372; AAC60727.1; -.
DR HSSP; P11362; LFCK
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SW00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR ATP-binding; Kinase; Transferrase; Tyrosine-protein kinase.
KW ATP-binding; Kinase; Transferrase; Tyrosine-protein kinase.
FT NON_TER
SQ SEQUENCE 567 AA; 63390 MW; C6D9CBA7ADF725E1 CRC64;

Query Match 85.2%; Score 46; DB 15; Length 567;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEXYLPQOGF 10
Db 439 DEYLPHQGF 448

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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=C3H/101, 129/SVJ, and 129/SvEvTAC;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
Sincclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
Mailhe N.J.;
"Comparative genomic sequence analysis and isolation of human and
mouse alternative Egr transcripts encoding truncated receptor
isoforms";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
[2]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J;
Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
Schnehl C., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
Mailhe N.J.;
"Comparative genomic sequence analysis and isolation of human and
mouse alternative Egr transcripts encoding truncated receptor
isoforms";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF275366; AAG28045.1; -.
EMBL; AF275364; AAG28045.1; JOINED.
EMBL; AF275365; AAG28045.1; JOINED.
EMBL; AF275367; AAG24386.1; -.
HSP; P11362; IFGK.
MGD; MGI:95294; Egfr.
InterPro: IPR000345; Cyto_heme_bind.
InterPro: IPR000494; EGFR_L_domain.
InterPro: IPR006211; Furin-like.
InterPro: IPR006212; Furin-repeat.
InterPro: IPR00719; Prot_kinase.
InterPro: IPR001245; Tyr_pkinase.
Pfam: PF00757; Furin-like; 1.
Pfam: PF00069; pkinase; 1.
Pfam: PF01030; Recep_L_domain; 2.
PRINTS; PR00109; TYRKINASE.
PRODOM; PD000001; Prot_kinase; 1.
SMART; SM00261; FU; 3.
SMART; SM00219; TYRKC; 1.
PROSITE; PS00190; CYTOCHROME_C; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
ATP-binding; Kinase; Receptor; Transferase; Tyrosine-protein kinase.
KW ATP-binding; Kinase; Receptor; Transferase; Tyrosine-protein kinase.
SQ SEQUENCE 1210 AA; 134840 MW; 62CD021C9DE32E18 CRC64;

Query Match 87.0%; Score 47; DB 11; Length 1210;
Best Local Similarity 80.0%; Pred. No. 1.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEYLVPQQGF 10
DB 1016 DEYLTPQQGF 1025

RESULT 9
Q85468 PRELIMINARY; PRT; 545 AA.
ID Q85468
AC Q85468;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Avian erythroblastosis virus (Ts34) v-erbB gene.
OS Avian erythroblastosis virus.
OC Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
NCBI_TaxID=11861;
RN [1]

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RESULT 11
Q06712          PRELIMINARY;          PRT;    729 AA.
ID  Q06712
AC  Q06712;
DT  01-NOV-1996 (TREMBlrel. 01, Created)
DT  01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT  01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE  Polyprotein.
GN  POLYPROTEIN.
OS  Avian rous-associated virus type 1.
OC  Viruses; Retrod viruses; Retroviridae; Alpharetrovirus.
OX  NCBI_TaxID=11950;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=94203659; PubMed=8152791;
RA  Vennstrom B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V.,
   Johnson A., Beug H.;
RT  "Retroviral capture of c-erbB proto-oncogene sequences: rapid
   evolution of distinct viral genomes carrying mutant v-erbB genes with
   different transforming capacities.";
RL  Oncogene 9:1307-1320(1994).
DR  EMBL; S89372; AAC60725.1; -.
DR  HSSP; P03322; 1A6S.
DR  InterPro; IPR000719; Prot_kinase.
DR  InterPro; IPR004028; Retro_M.
DR  InterPro; IPR001245; Tyr_kinase.
DR  Pfam; PF00069; pkinase; 1.
DR  Pfam; PF02813; Retro_M; 1.
DR  PRINTS; PR00109; TYRKINASE.
DR  ProDom; PD000001; Prot_kinase; 1.
DR  SMART; SM00219; TyRKc; 1.
DR  PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR  PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR  PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW  ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
SQ  SEQUENCE 729 AA; 80649 MW; 84D2F6914EFE1D63 CRC64;

Query Match      85.28; Score 46; DB 15; Length 729;
Best Local Similarity 80.08; Pred. No. 1.5;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy  1 EYLVPOQGF 10
   :||||| |||
Db  588 DEYLVPHQGF 597

RESULT 12
Q064895          PRELIMINARY;          PRT;    962 AA.
ID  Q064895
AC  Q064895;
DT  01-NOV-1996 (TREMBlrel. 01, Created)
DT  01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT  01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE  Gag, v-erb-A, v-erb-B protein.
GN  GAG, V-ERB-A, V-ERB-B.
OS  Avian erythroblastosis virus.
OC  Viruses; Retrod viruses; Retroviridae; Avian type C retroviruses.
OX  NCBI_TaxID=11861;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=90206603; PubMed=1969616;
RA  Bruskina A., Jackson J., Bishop J.M., McCarley D.J., Schatzman R.C.;
RT  "Six amino acids from the retroviral gene gag greatly enhance the
   transforming potential of the oncogene v-erb-B.";
RL  Oncogene 5:15-24(1990).
CC  -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC  -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
DR  EMBL; X52209; CAA36459.1; -.
DR  EMBL; X52211; CAA36459.1; JOINED.
DR  HSSP; P10828; 2NLL.
DR  InterPro; IPR000536; Hormone_rec_lig.
DR  InterPro; IPR000719; Prot_kinase.

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DR  InterPro; IPR001723; Stdhrmn_receptor.
DR  InterPro; IPR001245; Tyr_kinase.
DR  InterPro; IPR001628; Znf_C4steroid.
DR  Pfam; PF00104; hormone_rec; 1.
DR  Pfam; PF00069; pkinase; 1.
DR  Pfam; PF00105; zf-C4; 1.
DR  PRINTS; PR00398; STRDHORMONER.
DR  PRINTS; PR00047; STROIDFINGER.
DR  PRINTS; PR00109; TYRKINASE.
DR  ProDom; PD000001; Prot_kinase; 1.
DR  ProDom; PD000035; Znf_C4steroid; 1.
DR  SMART; SM00430; HOLI; 1.
DR  SMART; SM00219; TyRKc; 1.
DR  SMART; SM00399; Znf_C4; 1.
DR  PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR  PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR  PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR  PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW  ATP-binding; DNA-binding; Kinase; Metal-binding; Nuclear protein;
   Receptor; Transcription; Transcription regulation; Transferase;
   Tyrosine-protein kinase; Zinc; Zinc-finger.
SQ  SEQUENCE 962 AA; 108320 MW; 3C5AED791E4E95CE CRC64;

Query Match      85.28; Score 46; DB 15; Length 962;
Best Local Similarity 80.08; Pred. No. 2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy  1 EYLVPOQGF 10
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Db  856 DEYLVPHQGF 865

RESULT 13
Q032739          PRELIMINARY;          PRT;    876 AA.
ID  Q032739
AC  Q032739;
DT  01-JAN-1998 (TREMBlrel. 05, Created)
DT  01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT  01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE  ADP-ribosyltransferase.
GN  CDTB.
OS  Clostridium difficile.
OC  Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC  Clostridium.
OX  NCBI_TaxID=1496;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  STRAIN=CD196;
RX  MEDLINE=97230316; PubMed=9119480;
RA  Perelle S., Gibert M., Bourlioux P., Corthier G., Popoff M.R.;
RT  "Production of a complete binary toxin (actin-specific ADP-
   ribosyltransferase) by Clostridium difficile CDI96.";
RL  EMBL; L76081; AAB67305.1; -.
DR  HSSP; P13423; 1ACC.
DR  InterPro; IPR003896; Anthrax_toxinB.
DR  Pfam; PF03495; Binary_toxB; 1.
DR  PRINTS; PR01391; BINARYTOXINB.
KW  Transferase.
SQ  SEQUENCE 876 AA; 98797 MW; 25E06E2D45CE2B3B CRC64;

Query Match      74.18; Score 40; DB 2; Length 876;
Best Local Similarity 66.78; Pred. No. 30;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy  2 EYLVPOQGF 10
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Db  696 DYLVPEQGF 704

RESULT 14
Q9KH41          PRELIMINARY;          PRT;    876 AA.
ID  Q9KH41

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AC Q9KH41;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE CdtB.
 GN CdtB.
 OS Clostridium difficile.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1496;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CCUG 20309;
 RA Chang S.Y., Song K.P.;
 RT "ADP-ribosylating Binary Toxin Genes of Clostridium difficile strain
 RT CCUG 20309";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF271719; AAF81761.1; -;
 DR HSSP; P13423; LACC.
 DR InterPro; IPR003896; Anthrax toxinB.
 DR Pfam; PF03495; Binary toxinB. 1.
 DR PRINTS; PR01391; BINARYTOXINB.
 DR SEQUENCE 876 AA; 98793 MW; 366D62F352E745A5 CRC64;

Query Match 74.1%; Score 40; DB 2; Length 876;
 Best Local Similarity 66.7%; Pred. No. 30;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPOQGF 10
 DB 696 DYLVPEQGY 704

RESULT 15

Q9Q9I5 PRELIMINARY; PRT; 910 AA.
 AC Q9Q9I5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE 100 kDa protein homolog (Fragment).
 OS Avian adenovirus type 8 (strain ATCC A-2A) (Fowl adenovirus 8).
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Aviadenovirus.
 OX NCBI_TaxID=66295;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CFA40;
 RA Johnson M.A., Pooley C.;
 RL "Fowl adenovirus serotype 8 hypervirulent strain CFA40.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF155911; AAF17336.1; -;
 DR InterPro; IPR003381; Adeno_100.
 DR Pfam; PF02438; adeno_100; 1.
 FT NON_TER 1
 SQ SEQUENCE 910 AA; 102772 MW; EB0BA4227ED2CEC CRC64;

Query Match 70.4%; Score 38; DB 12; Length 910;
 Best Local Similarity 66.7%; Pred. No. 78;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEYLVPOQG 9
 DB 855 EEFLPEQG 863

Search completed: July 28, 2003, 17:05:58
 Job time : 100 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2003, 17:02:20 ; Search time 29 Seconds
(without alignments)
14,590 Million cell updates/sec

Title: US-09-930-125-3
Perfect score: 54
Sequence: 1 EYLVPPQGGF 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pap.*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pap.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pap.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pap.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pap.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	580	1	US-08-414-417B-69
2	54	100.0	580	2	US-08-486-348A-69
3	54	100.0	580	2	US-08-468-545B-69
4	54	100.0	580	3	US-08-466-680B-69
5	54	100.0	1255	1	US-08-467-083-68
6	54	100.0	1255	1	US-08-414-417B-68
7	54	100.0	1255	2	US-08-484-438-8
8	54	100.0	1255	2	US-08-486-348A-68
9	54	100.0	1255	2	US-08-625-101-2
10	54	100.0	1255	2	US-08-468-545B-68
11	54	100.0	1255	2	US-08-356-786-2
12	54	100.0	1255	3	US-08-466-680B-68
13	54	100.0	1255	4	US-09-527-487-2
14	50	92.6	13	1	US-08-128-971B-12
15	50	92.6	1210	2	US-08-484-438-7
16	50	92.6	1210	2	US-08-475-035-4
17	42	77.8	13	1	US-08-408-604A-69
18	37	68.5	512	3	US-09-356-818A-2
19	37	68.5	541	2	US-08-484-438-6
20	37	68.5	548	1	US-08-247-902A-2
21	37	68.5	548	5	PCT-US93-10541-2
22	37	68.5	687	5	PCT-US91-09784-2
23	37	68.5	705	2	US-08-456-647B-4
24	37	68.5	705	2	US-08-237-401A-4
25	37	68.5	1058	2	US-08-484-438-4
26	37	68.5	1308	2	US-08-484-438-2
27	36	66.7	9	5	PCT-US93-01669-56

28	36	66.7	209	4	US-09-252-991A-30648	Sequence 30648, A
29	35	64.8	516	4	US-09-215-694-16	Sequence 16, Appl
30	35	64.8	685	5	PCT-US91-09784-4	Sequence 4, Appl
31	34	63.0	182	4	US-09-328-352-8193	Sequence 8193, Ap
32	34	63.0	590	4	US-09-252-991A-19046	Sequence 19046, A
33	33	61.1	9	1	US-08-178-570-63	Sequence 63, Appl
34	33	61.1	9	3	US-08-369-643-63	Sequence 63, Appl
35	33	61.1	9	5	PCT-US95-00147-63	Sequence 63, Appl
36	33	61.1	12	1	US-08-406-192-1	Sequence 1, Appl
37	33	61.1	12	2	US-08-545-151-1	Sequence 1, Appl
38	33	61.1	12	6	5169933-12	Patent No. 5169933
39	33	61.1	27	6	5169933-43	Patent No. 5169933
40	33	61.1	371	4	US-09-252-991A-27127	Sequence 27127, A
41	33	61.1	442	2	US-08-821-355A-5	Sequence 5, Appl
42	33	61.1	442	2	US-09-003-687A-5	Sequence 5, Appl
43	33	61.1	442	3	US-09-136-605-5	Sequence 5, Appl
44	33	61.1	491	4	US-09-252-991A-29041	Sequence 29041, A
45	33	61.1	581	2	US-08-724-394A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-414-417B-69
; Sequence 69, Application US/08414417B
; Patent No. 5801005
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,417B
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-414-417B-69

Query Match 100.0%; Score 54; DB 1; Length 580;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EYLVPPQGGF 10
DB 346 EYLVPPQGGF 355

10267-10266 5801005
Paper
Reference - DP?

RESULT 2

US-08-486-348A-69
Sequence 69, Application US/08486348A
Patent No. 5846538

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

APPLICANT: Disis, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,348A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C6

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:

LENGTH: 580 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-486-348A-69

Query Match 100.0%; Score 54; DB 2; Length 580;

Best Local Similarity 100.0%; Pred. No. 0.029;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPQGF 10

|||||

Db 346 EYLVPQGF 355

RESULT 3

US-08-486-545B-69
Sequence 69, Application US/08468545B
Patent No. 5876712

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

APPLICANT: Disis, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

Query Match 100.0%; Score 54; DB 3; Length 580;

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,545B

FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C5

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:

LENGTH: 580 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-468-545B-69

Query Match 100.0%; Score 54; DB 2; Length 580;

Best Local Similarity 100.0%; Pred. No. 0.029;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPQGF 10

|||||

Db 346 EYLVPQGF 355

RESULT 4

US-08-466-680B-69

Sequence 69, Application US/08466680B

Patent No. 6075122

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

APPLICANT: Disis, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,680B

FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C4

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:

LENGTH: 580 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-466-680B-69

Query Match

100.0%; Score 54; DB 3; Length 580;

607512

DR for Sure

10267

Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPQGF 10
|||||
Db 346 EYLVPQGF 355

RESULT 5

US-08-467-083-68
; Sequence 68, Application US/08467083
; Patent No. 5726023
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,417
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIORITY INFORMATION:
; PRIORITY APPLICATION NUMBER: US 08/414,417
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELEPHONE: (206) 622-4900
; TELEX: 3723836 SEEDANBERRY
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

US-08-467-083-68
Query Match 100.0%; Score 54; DB 1; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPQGF 10
|||||
Db 1021 EYLVPQGF 1030

US-08-467-083-68
Query Match 100.0%; Score 54; DB 1; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPQGF 10
|||||
Db 1021 EYLVPQGF 1030

RESULT 6

US-08-414-417B-68
; Sequence 68, Application US/0841417B
; Patent No. 5801005
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,417B
FILING DATE: 31-MAR-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-414-417B-68
Query Match 100.0%; Score 54; DB 1; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYLVPQGF 10
|||||
Db 1021 EYLVPQGF 1030

US-08-414-438-8
; Sequence 8, Application US/08484438
; Patent No. 5811098
; Patent No. 5811098 5780031
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory D.
; APPLICANT: Culouscou, Jean-Michel
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Siegall, Clay B.
; APPLICANT: Hellstr m, Ingegerd
; APPLICANT: Hellstr m, Karl E.
; TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,438
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIORITY INFORMATION:
; PRIORITY APPLICATION NUMBER: 08/323,442
; FILING DATE: 14-OCT-1994
; APPLICATION NUMBER: US 08/150,704

RESULT 7

US-08-484-438-8
; Sequence 8, Application US/08484438
; Patent No. 5811098
; Patent No. 5811098 5780031
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory D.
; APPLICANT: Culouscou, Jean-Michel
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Siegall, Clay B.
; APPLICANT: Hellstr m, Ingegerd
; APPLICANT: Hellstr m, Karl E.
; TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,438
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIORITY INFORMATION:
; PRIORITY APPLICATION NUMBER: 08/323,442
; FILING DATE: 14-OCT-1994
; APPLICATION NUMBER: US 08/150,704

FILING DATE: 10-NOV-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/981,165
FILING DATE: 24-NOV-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 990-3090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-438-8

Query Match 100.0%; Score 54; DB 2; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPOQGF 10
Db 1021 EYLVPOQGF 1030

RESULT 8
US-08-486-348A-68
; Sequence 68, Application US/08486348A
; Patent No. 5846538
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0; Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486/348A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C6
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-486-348A-68

DP on

Query Match 100.0%; Score 54; DB 2; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPOQGF 10
Db 1021 EYLVPOQGF 1030

RESULT 9
US-08-625-101-2
; Sequence 2, Application US/08625101
; Patent No. 5869445
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
; TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
; TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
; TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0; Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/625/101
; FILING DATE: 01-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-625-101-2

5869445

DP for gene?

Query Match 100.0%; Score 54; DB 2; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPOQGF 10
Db 1021 EYLVPOQGF 1030

RESULT 10
US-08-468-545B-68
; Sequence 68, Application US/08468545B
; Patent No. 5876712
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0; Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468/545B
; FILING DATE: 01-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C8
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-468-545B-68

DP

ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,545B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-468-545B-68

Query Match 100.0%; Score 54; DB 2; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPOQGF 10
Db 1021 EYLVPOQGF 1030

RESULT 11
US-08-356-786-2

Sequence 2, Application US/08356786
Patent No. 5877305

GENERAL INFORMATION:

APPLICANT: Huston, James S.

APPLICANT: Oppermann, Hermann

APPLICANT: Houston, L. L.

APPLICANT: Ring, David B.

TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault

STREET: Exchange Place, 53 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/356,786

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/831,967

FILING DATE: 06-FEB-1992

ATTORNEY/AGENT INFORMATION:

NAME: Pitcher, Edmund R.

REGISTRATION NUMBER: 27,829

REFERENCE/DOCKET NUMBER: CRP-053

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-356-786-2

Query Match 100.0%; Score 54; DB 2; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPOQGF 10
Db 1021 EYLVPOQGF 1030

RESULT 12

US-08-466-680B-68

Sequence 68, Application US/08466680B

Patent No. 6075122

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

APPLICANT: Disis, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,680B

FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 68:

SEQUENCE CHARACTERISTICS:

LENGTH: 1255 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-466-680B-68

Query Match 100.0%; Score 54; DB 3; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPOQGF 10
Db 1021 EYLVPOQGF 1030

RESULT 13

US-09-527-487-2

Sequence 2, Application US/09527487

; Patent No. 6528060
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: HER2 ANTIGENIC PEPTIDES
; FILE REFERENCE: 126881309200
; CURRENT APPLICATION NUMBER: US/09/527,487
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-527-487-2

Query Match 100.0%; Score 54; DB 4; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.066; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 1 EYLVPPQGF 10
1021 EYLVPPQGF 1030

RESULT 14
US-08-128-971B-12
; Sequence 12, Application US/08128971B
; Patent No. 5525503
; GENERAL INFORMATION:
; APPLICANT: Christopher E. Rudd
; APPLICANT: Prasad Kanteti
; TITLE OF INVENTION: SIGNAL TRANSDUCTION VIA CD28
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55Sx
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/128,971B
; FILING DATE: September 28, 1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:
; NAME: Janis K. Fraser
; REGISTRATION NUMBER: 34,919
; REFERENCE/DOCKET NUMBER: 00530/073001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-128-971B-12

Query Match 92.6%; Score 50; DB 1; Length 13;
Best Local Similarity 80.0%; Pred. No. 0.0027; 0; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 0;

QY 1 EYLVPPQGF 10

Db 3 DEYLIPOQGF 12
:|||||

RESULT 15
US-08-484-438-7
; Sequence 7, Application US/08484438
; Patent No. 5811098
; Patent No. 5811098 5780031
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory D.
; APPLICANT: Culouscou, Jean-Michel
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Siegall, Clay B.
; APPLICANT: Hellstr m, Ingegerd
; APPLICANT: Hellstr m, Karl E.
; TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,438
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/323,442
; FILING DATE: 14-OCT-1994
; APPLICATION NUMBER: US 08/150,704
; FILING DATE: 10-NOV-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/981,165
; FILING DATE: 24-NOV-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-230
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1210 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-484-438-7

Query Match 92.6%; Score 50; DB 2; Length 1210;
Best Local Similarity 80.0%; Pred. No. 0.36;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYLVPPQGF 10
1014 DEYLIPOQGF 1023
:|||||

Search completed: July 28, 2003, 17:07:18
Job time : 30 secs